

07 634278

A

1	Q	I	V	L	T	Q	S	P	A	I	M	S	A	S	P	G	E	K	V	T
1	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	V	T
21	I	T	C	S	A	S	S	S	I		S	Y	M	H	W	F	Q	Q	K	P
21	I	T	C	R	A	S	Q	S	I	N	T	W	L	A	W	V	Q	Q	K	P
40	G	T	S	P	K	L	W	I	Y	T	T	S	N	L	A	S	G	V	P	A
41	G	K	A	P	K	L	L	<u>M</u>	Y	<u>K</u>	<u>A</u>	<u>S</u>	<u>S</u>	<u>L</u>	<u>E</u>	<u>S</u>	G	V	P	<u>S</u>
60	R	F	S	G	S	G	S	G	T	S	Y	S	L	T	I	S	R	M	E	A
61	R	F	<u>I</u>	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	P
80	E	D	A	A	T	Y	Y	C	H	Q	R	S	T	Y	P	L	T	F	G	S
81	D	D	F	A	T	Y	Y	C	<u>Q</u>	<u>Q</u>	<u>Y</u>	<u>N</u>	<u>S</u>	<u>D</u>	<u>S</u>	<u>K</u>	<u>M</u>	<u>F</u>	<u>G</u>	<u>Q</u>
100	G	T	K	L	E	L	K													
101	G	T	K	V	E	V	K													

1	Q	V	Q	L	Q	Q	S	G	A	E	L	A	K	P	G	A	S	V	K	M
1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V
21	S	C	K	A	S	G	<u>Y</u>	T	F	T	S	Y	R	M	H	W	V	K	Q	R
21	S	C	K	A	S	G	<u>G</u>	T	F	<u>S</u>	<u>R</u>	<u>S</u>	<u>A</u>	<u>I</u>	<u>I</u>	W	V	R	Q	A
41	P	G	Q	G	L	E	W	I	G	Y	I	N	P	S	T	G	Y	T	E	Y
41	P	G	Q	G	L	E	W	<u>M</u>	G	<u>G</u>	<u>I</u>	<u>V</u>	<u>P</u>	<u>M</u>	<u>F</u>	<u>G</u>	<u>P</u>	<u>P</u>	<u>N</u>	<u>Y</u>
61	N	Q	K	F	K	D	K	A	T	L	T	A	D	K	S	S	S	T	A	Y
61	<u>A</u>	<u>Q</u>	<u>K</u>	<u>F</u>	<u>Q</u>	<u>G</u>	<u>R</u>	<u>V</u>	T	I	T	A	D	E	S	T	N	T	A	Y
81	M	Q	L	S	S	L	T	F	E	D	S	A	V	Y	Y	C	A	R	G	
81	M	E	L	S	S	L	R	S	E	D	T	A	<u>F</u>	Y	<u>F</u>	C	A	<u>G</u>	<u>G</u>	<u>Y</u>
100	G	G	V	F	D	Y	W	G	Q	G	T	T	L	T	V	S	S			
101	<u>G</u>	<u>I</u>	<u>Y</u>	<u>S</u>	<u>P</u>	<u>E</u>	<u>E</u>	<u>Y</u>	<u>N</u>	G	<u>G</u>	L	V	T	V	S	S			

Figure 1

A

1	D	I	V	L	T	Q	S	P	<u>A</u>	S	L	A	V	S	L	G	Q	R	A	T
1	E	I	V	M	T	Q	S	P	<u>A</u>	T	L	S	V	S	P	G	E	R	A	T
21	I	S	C	R	A	S	Q	S	V	S	T	S	T	Y	N	Y	M	H	W	Y
21	L	S	C	R	A	S	Q	S	V	S	T	S	T	Y	N	Y	M	H	W	Y
41	Q	Q	K	P	G	Q	P	P	K	L	L	I	K	Y	A	S	N	L	E	S
41	Q	Q	K	P	<u>G</u>	<u>Q</u>	S	P	R	L	L	I	<u>K</u>	Y	A	S	N	L	E	S
61	G	V	P	A	R	F	S	G	S	G	F	G	T	D	F	T	L	N	I	H
61	G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S
81	P	V	E	E	E	D	T	V	T	Y	Y	C	Q	H	S	W	E	I	P	Y
81	<u>R</u>	<u>L</u>	<u>E</u>	S	E	D	F	A	V	Y	Y	C	<u>Q</u>	H	S	W	E	I	P	Y
101	T	F	G	G	G	T	K	L	E	I	K									
101	T	F	G	Q	G	T	R	V	E	I	K									
81	E	M	I	L	V	E	S	G	G	G	L	V	K	P	G	A	S	L	K	L
101	E	V	Q	L	L	E	S	G	G	G	L	V	Q	P	G	A	S	L	K	L
21	S	C	A	A	S	G	F	T	F	S	N	Y	G	L	S	W	V	R	Q	T
21	S	C	A	A	S	G	F	T	F	S	<u>N</u>	<u>Y</u>	<u>G</u>	<u>L</u>	<u>S</u>	W	V	R	Q	A
41	S	D	R	R	L	E	W	V	A	S	I	S	R	G	G	G	R	I	Y	S
41	P	G	K	G	L	E	W	V	A	<u>S</u>	<u>I</u>	<u>S</u>	<u>R</u>	<u>G</u>	<u>G</u>	<u>G</u>	<u>R</u>	<u>I</u>	<u>Y</u>	<u>S</u>
61	P	D	N	L	K	G	R	F	T	I	S	R	E	D	A	K	N	T	L	Y
61	<u>P</u>	<u>D</u>	<u>N</u>	<u>L</u>	<u>K</u>	<u>G</u>	R	F	T	I	S	R	N	D	S	K	N	T	L	Y
81	L	Q	M	S	S	L	K	S	E	D	T	A	L	Y	Y	C	L	R	E	G
81	L	<u>Q</u>	M	N	S	L	Q	A	E	D	T	A	L	Y	Y	C	<u>L</u>	R	<u>E</u>	<u>G</u>
101	I	Y	Y	A	D	Y	G	F	F	D	V	W	G	T	G	T	T	V	I	V
101	<u>I</u>	<u>Y</u>	<u>Y</u>	<u>A</u>	<u>D</u>	<u>Y</u>	<u>G</u>	<u>F</u>	<u>F</u>	<u>D</u>	<u>V</u>	<u>W</u>	<u>G</u>	<u>T</u>	<u>G</u>	<u>T</u>	<u>T</u>	<u>V</u>	<u>I</u>	<u>V</u>
121	S	S																		
121	S	S																		

Figure 2

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A

1	D	I	V	M	T	Q	S	H	K	F	M	S	T	S	V	G	D	R	V	S
1	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	V	T
21	I	T	C	K	A	S	Q	D	V	G	S	A	V	V	W	H	Q	Q	K	S
21	I	T	C	K	A	S	Q	D	V	G	S	A	V	V	W	<u>H</u>	Q	Q	K	P
41	G	Q	S	P	K	L	L	I	Y	W	A	S	T	R	H	T	G	V	P	D
41	G	K	A	P	K	L	L	<u>I</u>	Y	<u>W</u>	A	S	T	R	H	<u>T</u>	G	V	P	S
61	R	F	T	G	S	G	S	G	T	D	F	T	L	T	I	T	N	V	Q	S
61	R	F	<u>T</u>	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	P
81	E	D	L	A	D	Y	<u>F</u>	C	Q	Q	Y	S	I	F	P	L	T	F	G	A
81	D	D	F	A	T	Y	<u>F</u>	C	<u>Q</u>	<u>Q</u>	<u>Y</u>	<u>S</u>	<u>I</u>	<u>F</u>	<u>P</u>	<u>L</u>	<u>T</u>	<u>F</u>	<u>G</u>	<u>Q</u>
101	G	T	R	L	E	L	K													
101	G	T	K	V	E	V	K													

B

1	Q	V	Q	L	Q	Q	S	D	A	E	L	V	K	P	G	A	S	V	K	I
1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V
21	S	C	K	V	S	G	<u>Y</u>	T	F	T	D	H	T	I	H	W	M	K	Q	R
21	S	C	K	A	S	G	<u>Y</u>	T	F	<u>T</u>	<u>D</u>	<u>H</u>	<u>T</u>	<u>I</u>	<u>H</u>	W	<u>M</u>	R	Q	A
41	P	E	Q	G	L	E	W	<u>F</u>	G	Y	I	Y	P	R	D	G	H	T	R	Y
41	P	G	Q	G	L	E	W	<u>F</u>	G	<u>Y</u>	<u>I</u>	<u>Y</u>	<u>P</u>	<u>R</u>	<u>D</u>	<u>G</u>	<u>H</u>	<u>T</u>	<u>R</u>	<u>Y</u>
61	S	E	K	F	K	G	K	A	T	L	T	A	D	K	S	A	S	T	A	Y
61	<u>A</u>	<u>E</u>	<u>K</u>	<u>F</u>	<u>K</u>	<u>G</u>	<u>K</u>	<u>A</u>	<u>T</u>	<u>I</u>	<u>T</u>	<u>A</u>	<u>D</u>	<u>E</u>	<u>S</u>	<u>T</u>	<u>N</u>	<u>T</u>	<u>A</u>	<u>Y</u>
81	M	H	L	N	S	L	T	S	E	D	S	A	V	Y	F	C	A	R	G	R
81	M	E	L	S	S	L	R	S	E	D	T	A	<u>V</u>	Y	F	C	A	<u>R</u>	<u>G</u>	<u>R</u>
101	D	S	R	E	R	N	G	F	A	Y	<u>W</u>	<u>G</u>	<u>Q</u>	<u>G</u>	<u>T</u>	L	V	T	V	S
101	<u>D</u>	<u>S</u>	<u>R</u>	<u>E</u>	<u>R</u>	<u>N</u>	<u>G</u>	<u>F</u>	<u>A</u>	<u>Y</u>	<u>W</u>	<u>G</u>	<u>Q</u>	<u>G</u>	<u>T</u>	L	V	T	V	S
121	A																			
121	S																			

Figure 3

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A  
1  
21  
31  
41  
51  
61  
81  
81  
101  
101  
1  
21  
21  
41  
41  
61  
61  
81  
81  
101  
101

D	E	V	E	E	Q	S	S	A	S	L	A	V	S	L	G	Q	R	A	T	
D	E	Q	E	E	Q	S	S	A	<u>S</u>	L	A	S	A	S	V	G	Q	R	V	T
H	S	C	R	A	S	E	S	V	D	N	V	G	E	S	S	M	N	W	F	
H	S	C	R	A	S	E	S	V	D	N	V	G	E	S	S	M	N	W	<u>F</u>	
Q	Q	K	S	G	Q	S	S	X	L	L	H	V	A	A	S	N	Q	G	S	
Q	Q	K	S	G	X	A	S	X	L	L	<u>H</u>	V	A	A	S	N	Q	G	S	
G	V	S	A	R	S	S	G	S	G	S	G	T	D	F	S	L	N	I	H	
G	V	S	S	R	S	<u>S</u>	G	S	G	S	G	T	<u>D</u>	F	T	L	T	I	S	
P	M	E	E	D	D	T	A	M	Y	F	C	Q	Q	S	K	E	V	P	W	
S	L	Q	P	D	D	F	A	T	Y	Y	C	<u>Q</u>	<u>Q</u>	S	K	E	V	<u>P</u>	<u>W</u>	
T	F	G	G	G	T	K	L	E	I	K										
<u>T</u>	<u>F</u>	<u>G</u>	<u>Q</u>	<u>G</u>	<u>T</u>	<u>K</u>	<u>V</u>	<u>E</u>	<u>I</u>	<u>K</u>										
E	V	Q	L	Q	Q	S	G	P	E	L	V	K	P	G	A	S	V	K	I	
Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V	
S	C	K	A	S	G	<u>Y</u>	T	F	<u>T</u>	D	Y	N	M	H	W	V	K	Q	S	
S	C	K	A	S	G	<u>Y</u>	T	F	<u>T</u>	D	Y	N	M	H	W	V	R	Q	A	
H	G	K	S	L	E	W	<u>I</u>	G	Y	I	Y	S	Y	N	G	G	T	G	Y	
P	G	Q	G	L	E	W	<u>I</u>	G	<u>Y</u>	<u>I</u>	<u>Y</u>	<u>P</u>	<u>Y</u>	<u>N</u>	<u>G</u>	<u>G</u>	<u>T</u>	<u>G</u>	<u>Y</u>	
N	Q	K	F	K	S	K	A	T	L	T	V	D	N	S	S	S	T	A	Y	
N	Q	K	F	K	S	<u>K</u>	<u>A</u>	T	I	T	A	D	E	S	T	N	T	A	Y	
M	D	V	R	S	L	T	S	E	D	S	A	V	Y	Y	C	A	R	G	R	
M	E	L	S	S	L	R	S	E	D	T	A	<u>V</u>	<u>Y</u>	<u>Y</u>	C	A	<u>R</u>	<u>G</u>	<u>R</u>	
P	A	M	D	Y	W	G	Q	G	T	S	V	T	V	S	S					
P	A	M	D	<u>Y</u>	<u>W</u>	<u>G</u>	<u>Q</u>	<u>G</u>	<u>T</u>	L	V	T	V	S	S					

Figure 4

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A

1	2	1	7	1	2	3	3	3	A	1	M	S	A	S	3	G	E	K	V	T
11	U	1	2	X	3	2	3	3	3	3	L	S	<u>A</u>	S	7	G	J	R	V	T
11	M	3	3	3	G	3	3	3	7	3	3	M	Y	N	7	2	Q	R	P	G
41	1	3	3	<u>3</u>	G	3	3	3	7	3	3	M	Y	N	7	2	Q	K	P	G
41	S	S	3	3	L	L	1	Y	D	E	S	N	L	A	S	G	V	P	V	R
41	<u>X</u>	A	3	K	L	L	1	Y	D	E	S	N	L	A	S	G	V	P	S	R
61	F	S	G	S	G	S	G	3	S	<u>Y</u>	S	L	T	I	S	R	M	E	A	E
61	F	S	G	S	G	S	G	3	D	<u>Y</u>	T	3	T	I	S	S	L	Q	P	E
81	D	A	A	T	Y	Y	C	Q	Q	W	S	T	Y	P	L	T	F	G	A	G
81	D	I	A	T	Y	Y	C	Q	Q	W	S	T	Y	P	L	T	F	G	Q	G
101	T	K	L	E	L	K														
101	T	K	V	E	V	K														

B

1	Q	V	Q	L	K	Q	S	G	P	G	L	V	Q	P	S	Q	S	L	S	I
1	<u>E</u>	V	Q	L	L	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L
21	T	C	T	V	S	G	F	S	V	T	S	Y	G	V	H	W	I	R	Q	S
21	S	C	A	A	S	G	F	T	<u>Y</u>	<u>T</u>	<u>S</u>	<u>Y</u>	<u>G</u>	<u>V</u>	<u>H</u>	N	V	R	Q	A
41	P	G	K	G	L	E	W	L	G	V	I	W	S	G	G	S	T	D	Y	N
41	P	G	K	G	L	E	W	V	<u>G</u>	<u>V</u>	<u>I</u>	<u>W</u>	<u>S</u>	<u>G</u>	<u>G</u>	S	T	D	Y	N
61	A	A	F	I	S	R	L	T	I	S	K	D	N	S	K	S	Q	V	F	P
61	A	A	F	I	S	R	F	T	I	S	R	<u>D</u>	<u>N</u>	S	K	N	T	L	Y	L
81	K	V	N	<u>S</u>	L	Q	P	A	D	T	A	I	Y	Y	C	A	R	A	G	D
81	Q	M	N	<u>S</u>	L	Q	A	E	<u>D</u>	<u>T</u>	A	I	Y	Y	C	A	R	<u>A</u>	<u>G</u>	<u>D</u>
101	Y	N	Y	D	G	F	A	Y	W	G	Q	G	T	L	V	T	V	S	A	
101	<u>Y</u>	<u>N</u>	<u>Y</u>	<u>D</u>	<u>G</u>	<u>F</u>	<u>A</u>	<u>Y</u>	<u>W</u>	<u>G</u>	<u>Q</u>	<u>G</u>	<u>T</u>	<u>L</u>	<u>V</u>	<u>T</u>	<u>V</u>	<u>S</u>	<u>S</u>	

Figure 5

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A

1	D	I	V	L	T	Q	S	P	A	T	L	S	V	T	P	G	D	S	V	S
1	E	I	V	L	T	Q	S	P	G	T	L	S	L	S	P	G	E	R	A	T
21	L	S	C	R	A	S	Q	S	I	S	N	N	L	H	W	Y	Q	Q	K	S
21	L	S	C	R	A	S	Q	S	I	S	N	N	L	H	W	Y	Q	Q	K	P
41	H	E	S	P	R	L	L	I	K	Y	A	S	Q	S	I	S	G	I	P	S
41	G	Q	A	P	R	L	L	I	<u>K</u>	<u>Y</u>	<u>A</u>	<u>S</u>	<u>Q</u>	<u>S</u>	<u>I</u>	<u>S</u>	G	I	P	D
61	R	F	S	G	S	G	S	G	T	D	F	T	L	S	V	N	G	V	E	T
61	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	R	L	E	P
81	E	D	F	G	M	Y	F	C	Q	Q	S	N	S	W	P	H	T	F	G	G
81	E	D	F	A	V	Y	Y	C	<u>Q</u>	<u>Q</u>	<u>S</u>	<u>N</u>	<u>S</u>	<u>W</u>	<u>P</u>	<u>H</u>	<u>T</u>	<u>F</u>	<u>G</u>	<u>Q</u>
101	G	T	K	L	E	I	K													
101	G	T	K	V	E	I	K													

B

1	E	V	Q	L	<u>Q</u>	Q	S	G	P	E	L	V	K	K	P	G	A	S	M	K	I
1	Q	V	Q	L	<u>V</u>	Q	S	G	A	E	V	K	K	P	G	S	S	V	R	V	
21	S	C	K	A	S	V	Y	S	F	T	G	Y	T	M	N	W	V	K	Q	S	
21	S	C	K	<u>A</u>	S	G	<u>Y</u>	<u>S</u>	F	<u>T</u>	<u>G</u>	<u>Y</u>	<u>T</u>	<u>M</u>	<u>N</u>	<u>W</u>	<u>V</u>	<u>R</u>	<u>Q</u>	<u>A</u>	
41	H	G	Q	N	L	E	W	I	G	L	I	N	P	Y	N	G	G	T	S	Y	
41	P	G	K	G	L	E	W	V	G	<u>L</u>	<u>I</u>	<u>N</u>	<u>P</u>	<u>Y</u>	<u>N</u>	<u>G</u>	<u>G</u>	<u>T</u>	<u>S</u>	<u>Y</u>	
61	N	Q	K	F	K	G	K	A	T	L	T	V	D	K	S	S	N	T	A	Y	
61	<u>N</u>	<u>Q</u>	<u>K</u>	<u>F</u>	<u>K</u>	<u>G</u>	<u>R</u>	<u>V</u>	<u>T</u>	<u>V</u>	<u>S</u>	<u>L</u>	<u>K</u>	<u>P</u>	<u>S</u>	<u>F</u>	<u>N</u>	<u>Q</u>	<u>A</u>	<u>Y</u>	
81	M	E	L	L	S	L	T	S	A	D	S	A	V	Y	Y	C	T	R	R	G	
81	M	E	L	S	S	L	F	S	E	D	T	A	V	Y	Y	C	<u>T</u>	<u>R</u>	<u>R</u>	<u>G</u>	
101	F	R	D	Y	S	M	D	Y	W	G	Q	G	T	S	V	T	V	S	S		
101	<u>F</u>	<u>R</u>	<u>D</u>	<u>Y</u>	<u>S</u>	<u>M</u>	<u>D</u>	<u>Y</u>	<u>W</u>	<u>G</u>	<u>Q</u>	<u>G</u>	<u>T</u>	<u>L</u>	<u>V</u>	<u>T</u>	<u>V</u>	<u>S</u>	<u>S</u>		

Figure 6

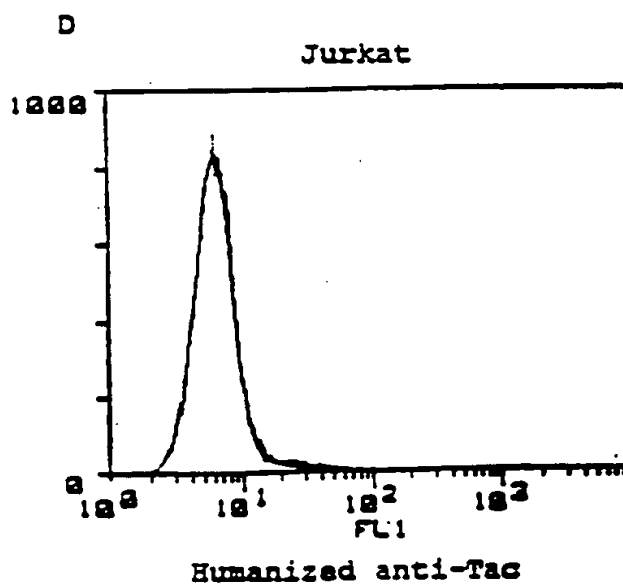
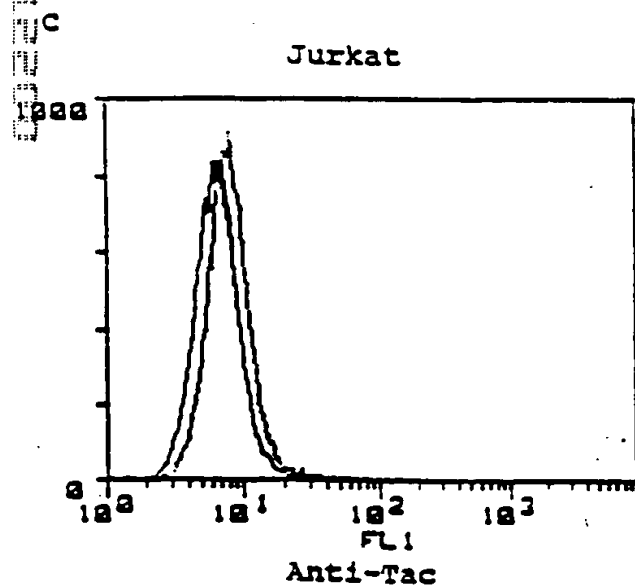
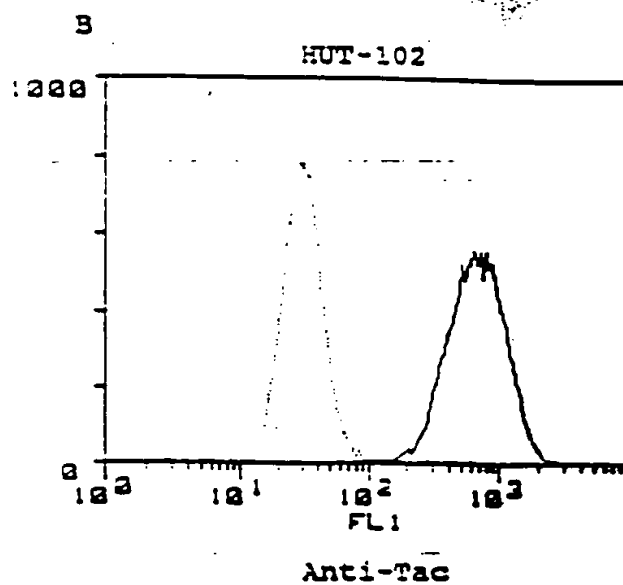
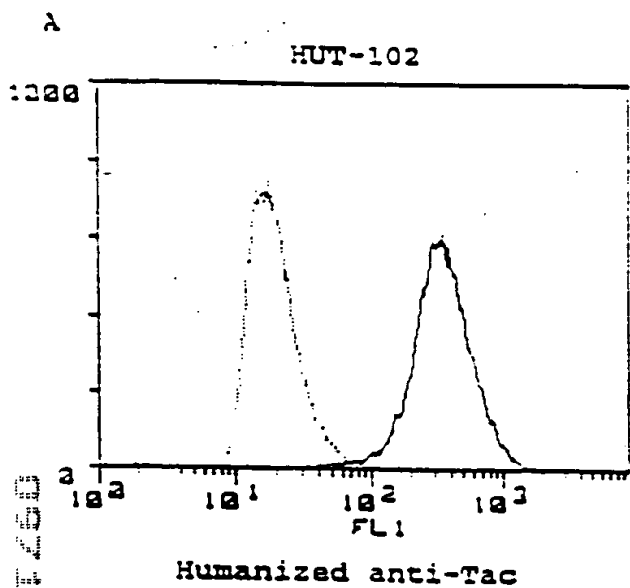
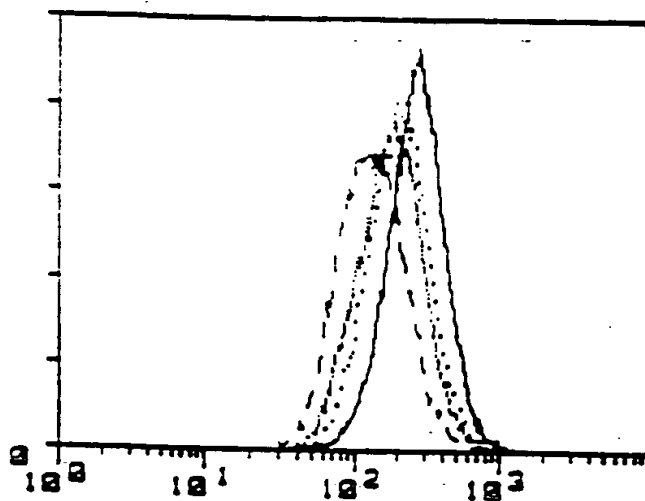


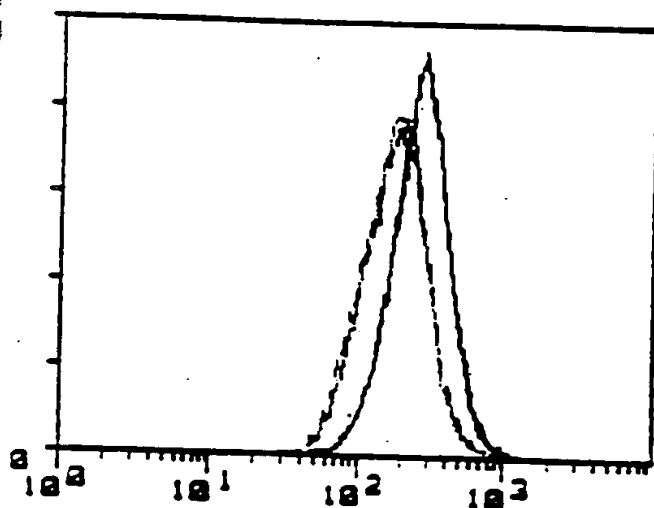
Figure 7

A



— 0 ng anti-Tac  
..... 10 ng  
----- 20 ng  
- . - . - 40 ng

002211-5669-260

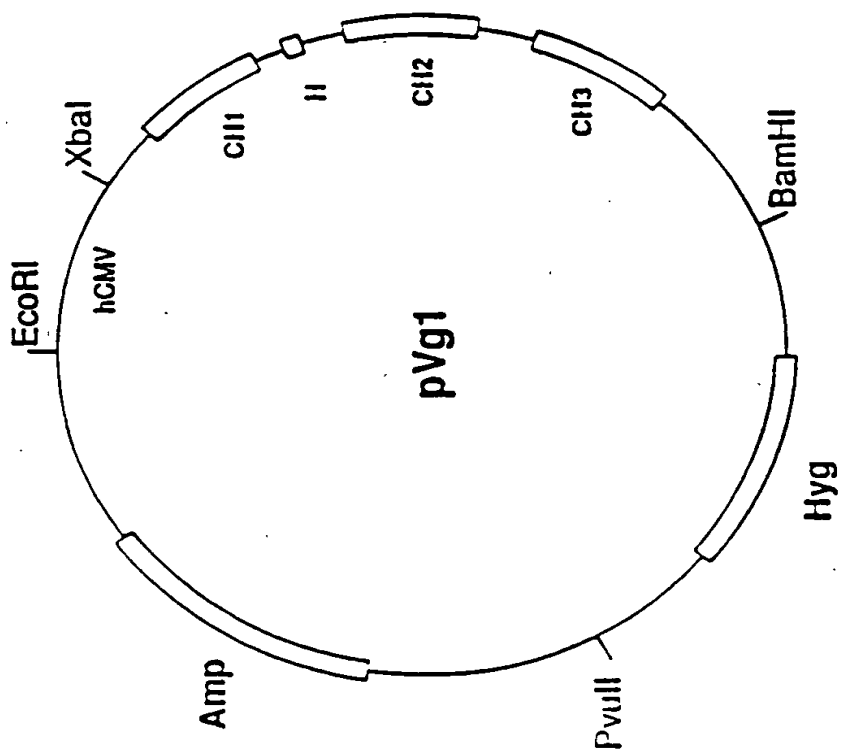


— 0 ng anti-Tac  
..... 20 ng anti-Tac  
- . - . - 20 ng humanized anti-Ta

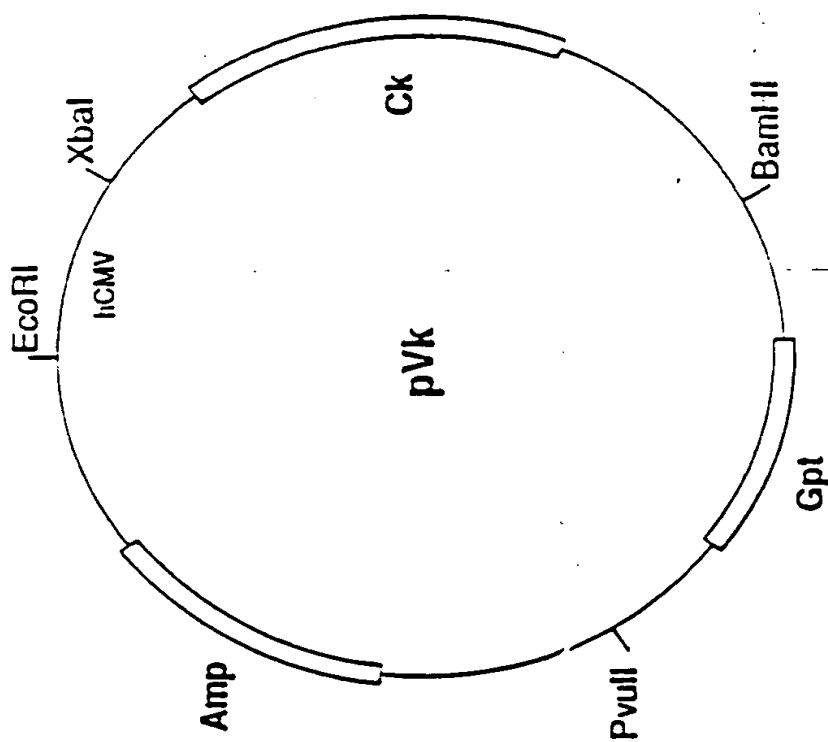
Figure 8



10(A)



(B)



## Figure 9

A.

Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V
Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V
S	C	K	A	S	G	<u>Y</u>	T	F	<u>T</u>	S	Y	R	M	H	W	V	R	Q	A
S	C	K	A	S	G	<u>G</u>	T	F	<u>S</u>	S	Y	R	M	H	W	V	R	Q	A
P	G	Q	G	L	E	W	<u>I</u>	G	Y	I	N	P	S	T	G	Y	T	E	Y
P	G	Q	G	L	E	W	<u>M</u>	G	Y	I	N	P	S	T	G	Y	T	E	Y
N	Q	K	F	K	D	<u>K</u>	<u>A</u>	T	I	T	A	D	E	S	T	N	T	A	Y
N	Q	K	F	K	D	<u>R</u>	<u>V</u>	T	I	T	A	D	E	S	T	N	T	A	Y
M	E	L	S	S	L	R	S	E	D	T	A	<u>V</u>	Y	<u>Y</u>	C	A	<u>R</u>	Q	Q
M	E	L	S	S	L	R	S	E	D	T	A	<u>F</u>	Y	<u>F</u>	C	A	<u>G</u>	<u>G</u>	<u>Q</u>
G	V	F	D	Y	<u>W</u>	<u>G</u>	<u>Q</u>	G	<u>T</u>	L	V	T	V	S	S				
G	V	F	D	Y	<u>E</u>	<u>Y</u>	<u>N</u>	G	<u>G</u>	L	V	T	V	S	S				

B.

D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	V	T
D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	V	T
I	T	C	S	A	S	S	S	S	I	S	Y	M	H	W	Y	Q	Q	K	P
I	T	C	S	A	S	S	S	S	I	S	Y	M	H	W	Y	Q	Q	K	P
K	A	P	K	L	L	<u>I</u>	Y	T	T	S	N	L	A	S	G	V	P	<u>A</u>	R
K	A	P	K	L	L	<u>M</u>	Y	T	T	S	N	L	A	S	G	V	P	<u>S</u>	R
F	<u>S</u>	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	P	D
F	<u>I</u>	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	P	D
D	F	A	T	Y	Y	C	H	Q	R	S	T	Y	P	L	T	F	G	Q	G
D	F	A	T	Y	Y	C	H	Q	R	S	T	Y	P	L	T	F	G	Q	G
T	K	V	E	V	K														
T	K	V	E	V	K														

Figure 10

A.

10	20	30	40	50	60	70
AGCTTCTAGA	TGGCATGGAG	CTGGATCTTT	CTCTTCCTCC	TGTCAGGTAC	CGCGGGCGTG	CAGTCTCAAG
TCGAAGATCT	ACCCTACCTC	GACCTAGAAA	GAGAAGGAGG	ACAGTCCATG	CGCGCCGCAC	GTOAGAGTCC
80	90	100	110	120	130	140
TCCAGCTTGT	CCAGTCTGGG	GCTGAAGTCA	AGAAACCTGG	CTCGAGCGTG	AAGGTCTCCT	GCAAAGGCTTC
AGGTGGAACA	GGTCAGACCC	CGACTTCAGT	TCTTTGGACC	GAGGTGCGAC	TTCCAQAGGA	CGTTCCGAAG
150	160	170	180	190	200	210
TGGCGGGACC	TTTTCTAGCT	ACAGGATGCA	CTGGGTAAGG	CAGGCCCCCTG	GACAGGGTCT	GGAATGATG
ACGCGCGCTG	AAAAGATCGA	TGTCTTACGT	GACCCATTCC	GTCCGGGGAC	CTGTCCCAQA	CGTTACCTAC
220	230	240	250	260	270	280
GGATATATTA	ATCCGTGCGC	TGGGTATACT	GAATACAATC	AGAAAGTTCAA	GGACAGGGTC	ACAATTACTG
CCTATATAAT	TAGGCAGCTG	ACCCATATGA	CTTATGTTAG	TCTTCAAAGT	CCTGTCCCAQ	TGTTAATGAG
290	300	310	320	330	340	350
CACACGAATC	CACCAATACA	CCCTACATGG	AACTGAGCAQ	CCTGAGATCT	GAGGACACCG	CATTCTATTT
GTCTGCTTAG	GTOGTTATGT	CGGATGTACC	TTGACTCGTC	GGACTCTAGA	CTCCTGTGGC	GTAAGATAAA
360	370	380	390	400	410	420
CTGTGCAAGG	GGTGGGGGAG	TCTTTGACTA	CGAATACAAT	GGAGGGCTGG	TCACAGTCTC	CTCAAGGTGAG
GACAGGTCCC	CCACCCCGCT	AGAAACTGAT	GCTTATGTTA	CCTCCCGACC	AGTGTCAQAG	GAOTCCAGTC
430	440					
TCCTTAAAAC	CTCTAGACGA	TAT				
AGGAATTTTG	GAGATCTGCT	ATA				

B.

10	20	30	40	50	60	70
CAAATCTAGA	TGGAGACCGA	TACCTCTCTG	CTATGGGTCC	TCCTGCTATG	GGTCCCAGGA	TCAACCGGAG
GTTTAGATCT	ACCTCTGGCT	ATGGGAGGAC	GATACCCAGG	AGGACGATAC	CCAAGGTCTT	AGTTGGCCTC
80	90	100	110	120	130	140
ATATTGAGAT	CACCCAGTCT	CCATCTACCC	TCTCTGCTAG	CGTGGCGGAT	AGGGTCACCA	TAACCTGCTC
TATAAGTCTA	CTGGGTCAGA	GGTAAGATGG	AGAGACGATC	GCAGCCCTTA	TCCAGTGGGT	ATTGGAGGAG
150	160	170	180	190	200	210
TGCCAGCTCA	AGTATAAGTT	ACATGCACTG	GTACCAGCAG	AAOCCAGGCA	AAGCTCCCAA	GCTTCTAATG
ACGGTGGAGT	TCATATTCAA	TGTACGTOAC	CATGGTCTGC	TTGGGTCCGT	TTGGAGGGGT	CGAAAGATTAG
220	230	240	250	260	270	280
TATACCACAT	CCAACCTGGC	TTCTGGAGTC	CCTTCTCGCT	TCATTGGCAG	TGGATCTGGG	ACCGAGTTCA
ATATGGTGTA	GGTTGGACCG	AAGACCTCAG	GGAAAGACGA	AGTAACCGTC	ACCTAGACCC	TGCTCAAGT
290	300	310	320	330	340	350
CCCTCACAAT	CAGCTCTCTG	CAQCCAGATG	ATTTGCGCAC	TTATTACTGC	CATCAAAGGA	GTACTTACCC
GGGAGTGTTA	GTCCGAGAGAC	GTCCGTCTAC	TAAAGCGGTG	AATAATGACG	GTAATTTCTT	CATGAATGGG
360	370	380	390	400		
ACTCACGTTT	GGTCAGGGGA	CCAAGGTGGA	GGTCAAACGT	AAGTACACTT	TTCTAGATAT	A
TGAGTGCAAQ	CCAGTCCCTT	GTTCCACCT	CCAATTTGCA	TTATGTGAA	AAGATCTATA	T

Figure 11

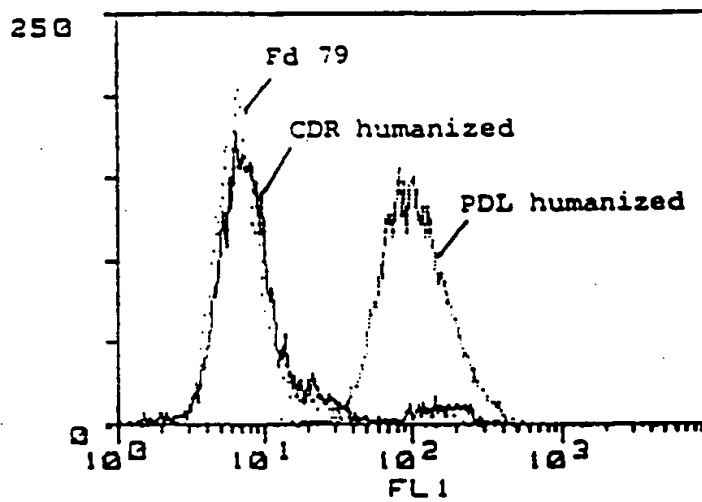


Figure 12

07 634278

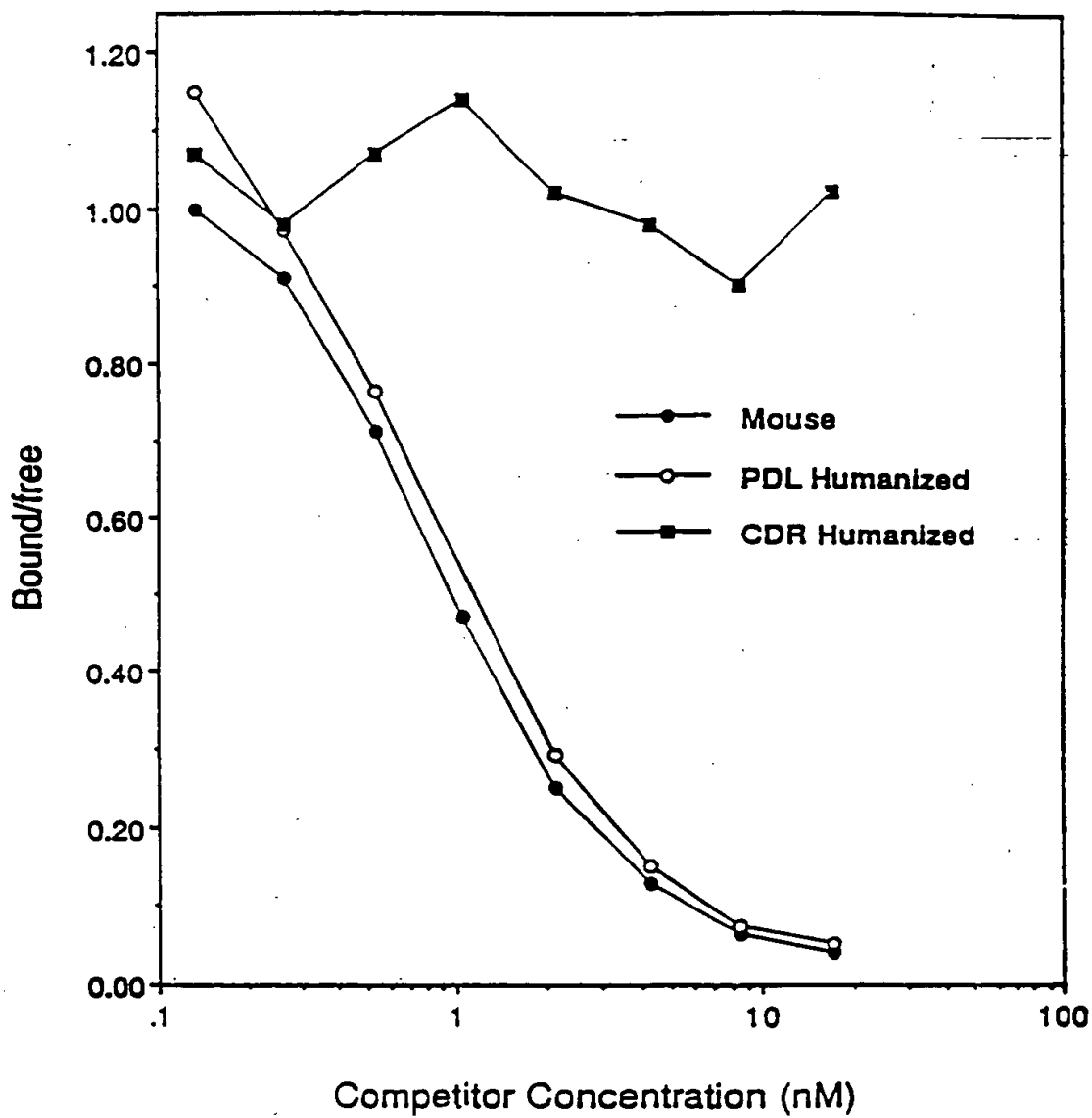


Figure 13

07 634278

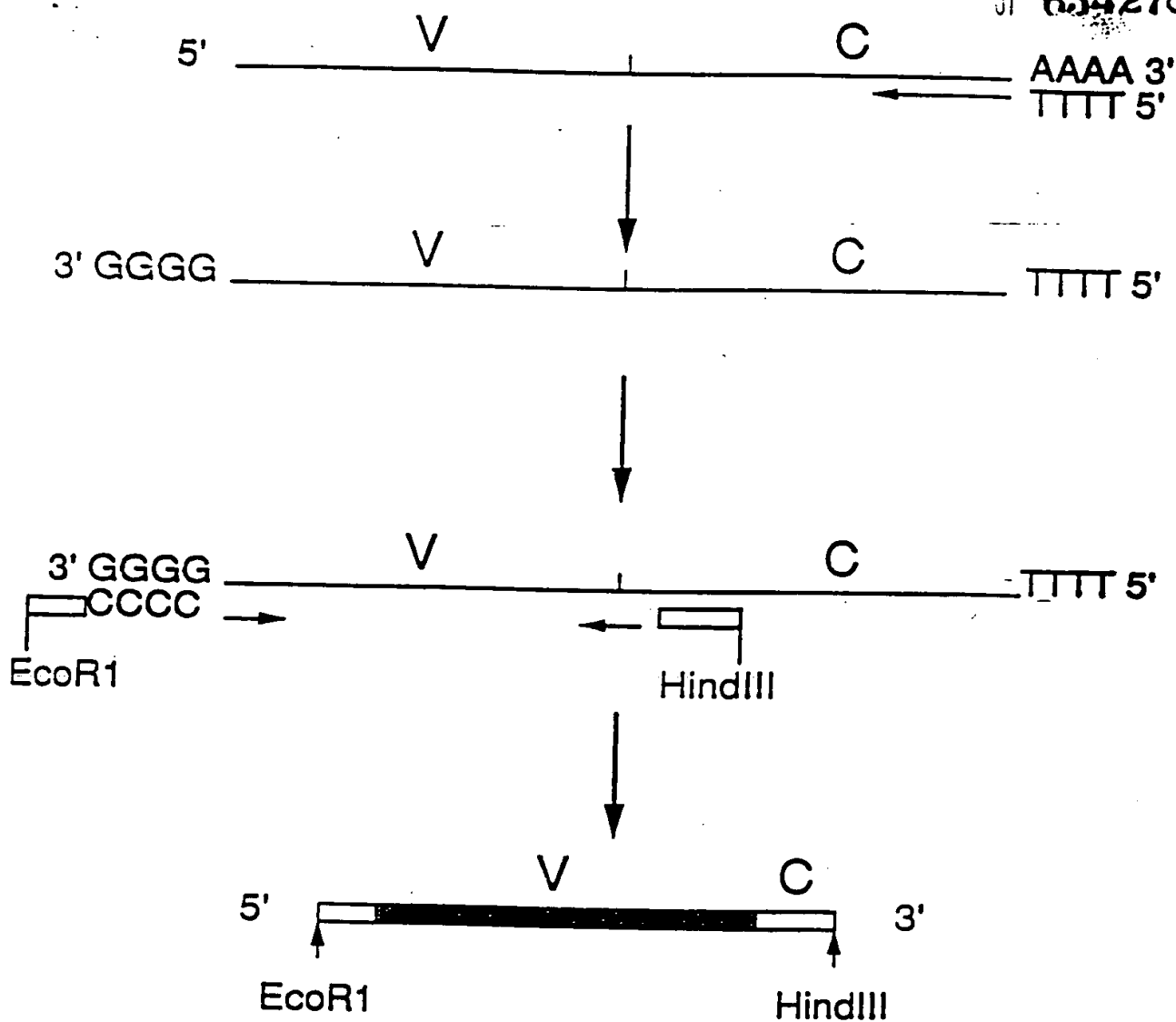


Figure 14

07 634278

1	Q	V	Q	L	Q	Q	S	G	A	E	L	A	K	P	G	A	S	V	K	M
1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V
21	S	C	K	A	S	G	V	F	F	F	S	V	R	M	H	W	V	K	Q	R
21	S	C	K	A	S	G	G	F	F	S	R	S	A	F	F	W	V	R	Q	A
							*			*										
41	P	G	Q	G	L	E	W	F	G	V	F	N	P	S	F	G	V	F	E	Y
41	P	G	Q	G	L	E	W	M	G	G	F	V	P	M	F	G	P	P	N	Y
							*													
61	N	Q	K	F	K	D	K	A	T	L	T	A	D	K	S	S	S	T	A	Y
61	A	Q	K	F	Q	G	R	V	T	I	T	A	D	E	S	T	N	T	A	Y
							*	*												
81	M	Q	L	S	S	L	T	F	E	D	S	A	V	Y	Y	C	A	R	G	
81	M	E	L	S	S	L	R	S	E	D	T	A	F	Y	F	C	A	G	G	Y
											*		*		*		*			
100	G	G	V	F	D	Y	W	G	Q	G	T	T	L	T	V	S	S			
101	G	F	Y	S	P	E	E	Y	N	G	G	L	V	T	V	S	S			
							*	*	*	*	*									

FIGURE 15

07 634278

1	Q	I	V	L	F	Q	S	F	A	F	M	S	A	S	P	G	E	K	V	T
1	D	I	Q	M	F	Q	S	F	S	F	L	S	A	S	V	G	C	R	V	T
21	I	F	C	S	A	S	S	S	I		S	V	M	H	N	F	Q	Q	K	P
21	I	I	C	R	A	S	Q	S	I	N	F	H	L	A	H	V	Q	Q	K	P
40	G	F	S	P	K	L	W	I	Y	F	F	S	N	L	A	S	G	V	P	A
41	G	X	A	P	K	L	L	M	Y	X	A	S	S	L	E	S	G	V	P	S
60	R	F	S	G	S	G	S	G	F	S	V	S	L	F	I	S	R	M	E	A
61	R	F		G	S	G	S	G	F	E	F	F	L	F	I	S	S	L	Q	P
80	E	D	A	A	F	Y	Y	C	H	Q	R	S	F	V	P	L	F	F	G	S
81	D	D	F	A	F	Y	Y	C	Q	Q	Y	N	S	D	S	K	M	F	G	Q
100	G	F	K	L	E	L	K													
101	G	F	K	V	E	V	K													

FIGURE 16



10 20 30 40 50 60  
TCTAGATGGGATGGAGCTGGATCTTTCTCTTCCTCCTGTCAGGTACCGCGGGCGTGAAGT  
M G W S W I F L F L L S G T A G V H

70 80 90 100 110 120  
CTCAGGTCCAGCTTGTCCAGTCTGGGGCTGAAGTCAAGAAACCTGGCTCGAGCGTGAAGG  
S Q V Q L V Q S G A E V K K P G S S V K

130 140 150 160 170 180  
TCTCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACAGGATGCAGTGGGTAAGGCAGG  
V S C K A S G Y T F T S Y R M H W V R Q

190 200 210 220 230 240  
CCCCTGGACAGGGTCTGGAATGGATTGGATATATTAATCCGTCCGACTGGGTATACTGAAT  
A P G Q G L E W I G Y I N P S T G Y T E

250 260 270 280 290 300  
ACAATCAGAAGTTCAAGGACAAGGCAACAATTACTGCAGACGAATCCACCAATACAGCCT  
Y N Q K F K D K A T I T A D E S T N T A

310 320 330 340 350 360  
ACATGGAACTGAGCAGCCTGAGATCTGAGGACACCGCAGTCTATTACTGTGCAAGAGGGG  
Y M E L S S L R S E D T A V Y Y C A R G

370 380 390 400 410 420  
GGGGGGTCTTTGACTACTGGGGCCAAGGAACCCTGGTCACAGTCTCCTCAGGTGAGTCCT  
G G V F D Y W G Q G T L V T V S S

430  
TAAAACCTCTAGA

FIGURE 17

10 20 30 40 50 60  
TCTAGATGGAGACCGATACCCCTCCTGCTATGGGTCCCTCCTGCTATGGGTCCCGAGGATCAA  
M E T D T L L L W V L L L W V P G S

70 80 90 100 110 120  
CCGGAGATATTCAGATGACCCAGTCTCCATCTACCCCTCTCTGCTAGCGTCGGGGATAGGG  
T G D I Q M T Q S P S T L S A S V G D R

130 140 150 160 170 180  
TCACCATAACCTGCTCTGCCAGCTCAAGTATAAGTTACATGCACTGGTACCAGCAGAAGC  
V T I T C S A S S S I S Y M H W Y Q Q K

190 200 210 220 230 240  
CAGGCAAAGCTCCCAAGCTTCTAATTTATACCACATCCAACCTGGCTTCTGGAGTCCCTG  
P G K A P K L L I Y T T S N L A S G V P

250 260 270 280 290 300  
CTCGCTTCAGTGGCAGTGGATCTGGGACCGAGTTCACCCTCACAATCAGCTCTCTGCAGC  
A R F S G S G S G T E F T L T I S S L Q

310 320 330 340 350 360  
CAGATGATTTTCGCCACTTATTACTGCCATCAAAGGAGTACTTACCCACTCACGTTCCGGTC  
P D D F A T Y Y C H Q R S T Y P L T F G

370 380 390 400  
AGGGGACCAAGGTGGAGGTCAAACGTAAGTACACTTTTCTAGA  
Q G T K V E V K

FIGURE 18

07 634278

A

HES12 AGCTTCTAGATGGGATGGAGCTGGATCTTTCTCTTCCTCCTGTCAGGTACCCSCGGGCGTG  
CACTCTCAGGTCCAGCTTGTCCAGTCTGGGGCTGAAGTCAAGAAACCTGGCTCGAGCGTG  
AAGGTC

HES13 CCCAGTCGACGGATTAATATATCCAATCCATTCCAGACCCTGTCCAGGGGCCTGCCTTAC  
CCAGTGCATCCTGTAGCTAGTAAAGGTGTAGCCAGAAGCCTTGCCAGGAGACCTTCACGCT  
CGAGCCAGG

HES14 TATATTAATCCGTGCGACTGGGTATACTGAATACAATCAGAAGTTCAAGGACAAGGCAACA  
ATTACTGCAGACGAATCCACCAATACAGCCTACATGGAAGTGAAGCAGCCTGAGATCTGAG  
GACA

HES15 ATATCGTCTAGAGGTTTTAAGGACTCACCTGAGGAGACTGTGACCAGGGTTCCTTGGCCC  
CAGTAGTCAAAGACCCCCCCCCCTCTTGACAGTAATAGACTGCGGTGTCCTCAGATCTC  
AGGCTGCT

B

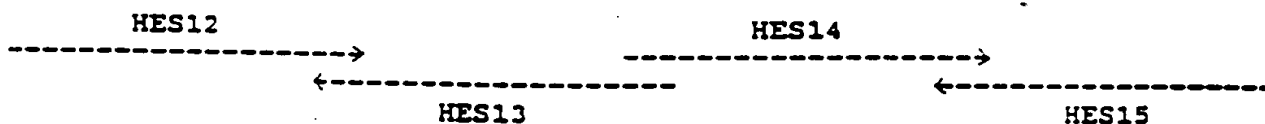


FIGURE 19

07 634278

A

JFD1 CAAATCTAGATGGAGACCGATACCCTCCTGCTATGGGTCTCTGCTATGGGTCCCAGGA  
TCAACCGAGATATTGAGATGACCCAGTCTCCATCTACCCTCTCTGCTAGCGTCGGGGAT

JFD2 ATAAATTAGAAGCTTGGGAGCTTTGCCTGGCTTCTGCTGGTACCAGTGCATGTAACCTTAT  
ACTTGAGCTGGCAGAGCAGGTTATGGTGACCCTATCCCCGACGCTAGCAGAGAG

JFD3 GCTCCCAAGCTTCTAATTTATACCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGCTTC  
AGTGGCAGTGGATCTGGGACCGAGTTCACCCTCACAATCAGCTCTCTGCAGCCAGATGAG  
TTC

JFD4 TATATCTAGAAAAGTGTAATTACGTTTGACCTCCACCTTGGTCCCCTGACCGAACGTGAG  
TGGGTAAGTACTCCTTTGATGGCAGTAATAAGTGGCGAAATCATCTGGCTGCAGAGAGCT  
GA

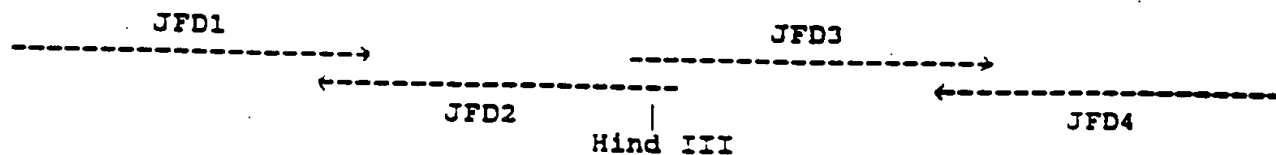


FIGURE 20

07 634278

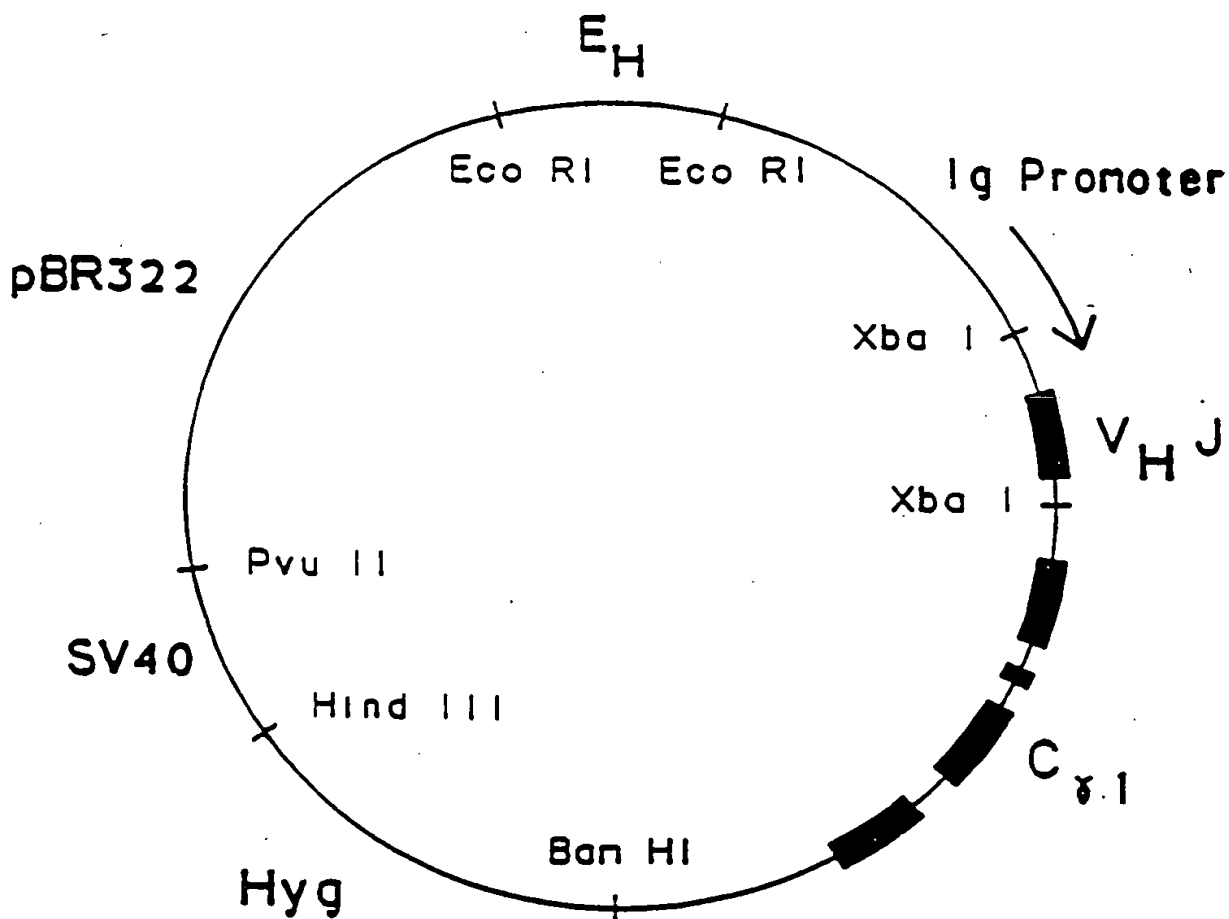


FIGURE 21

0074600-1100  
000000-000000

pBR322

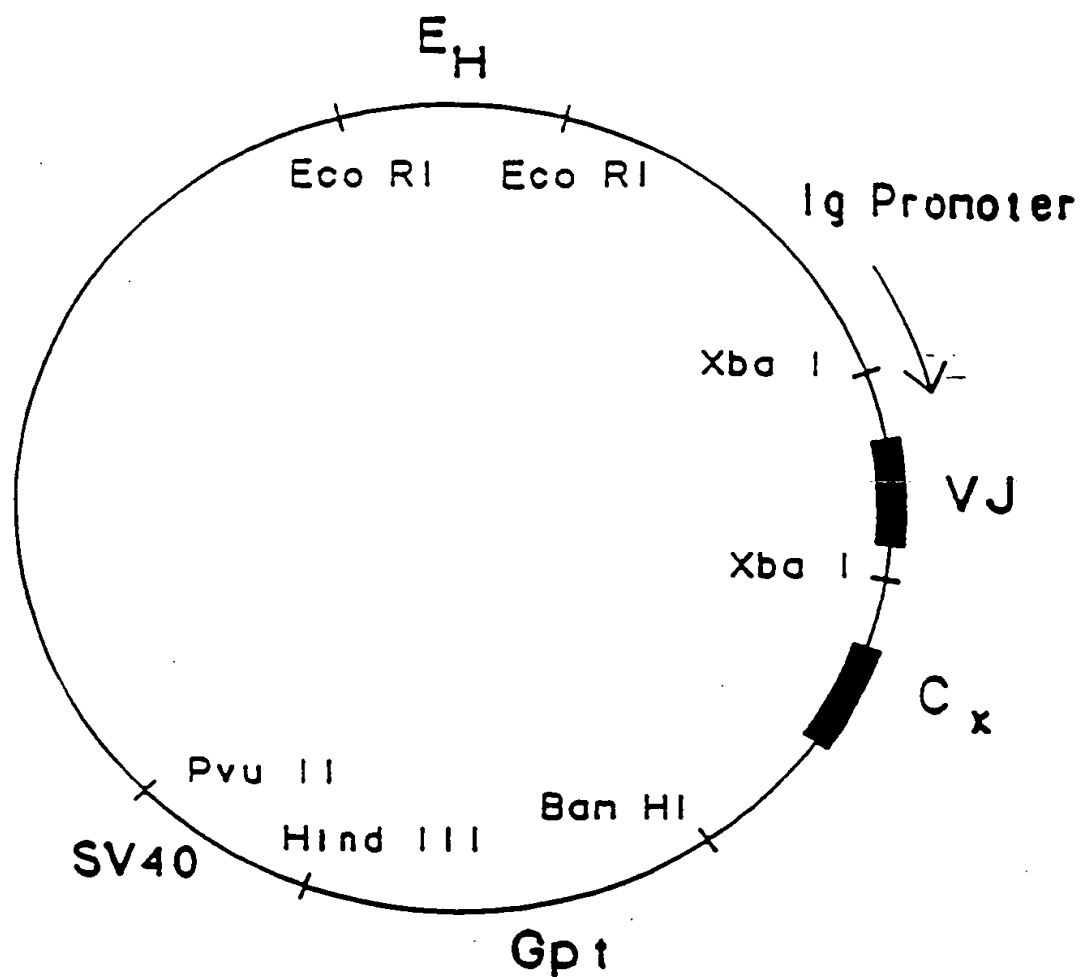


FIGURE 22

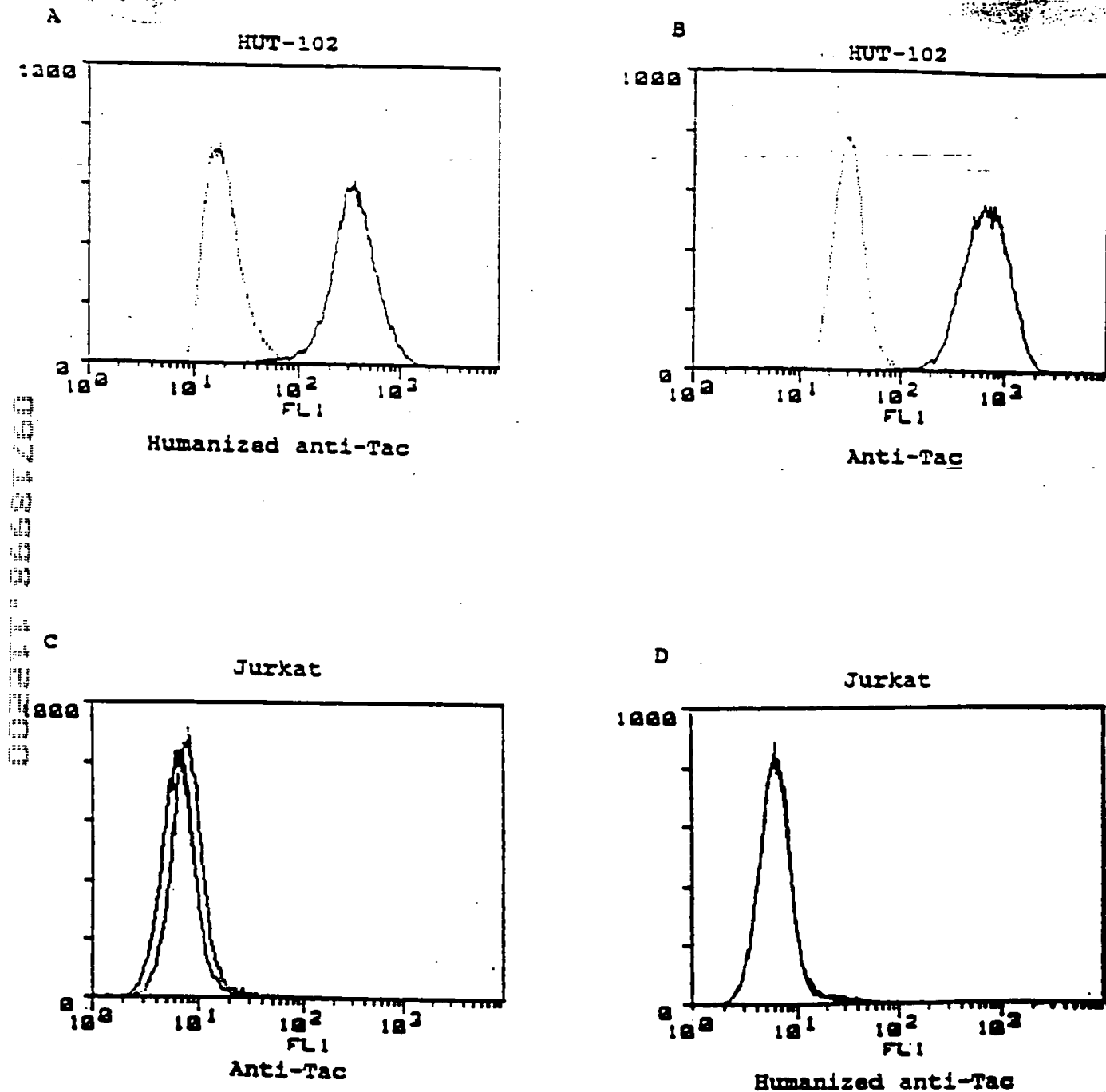
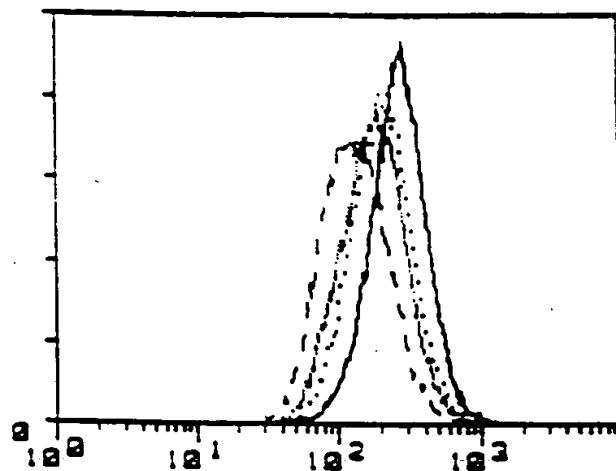


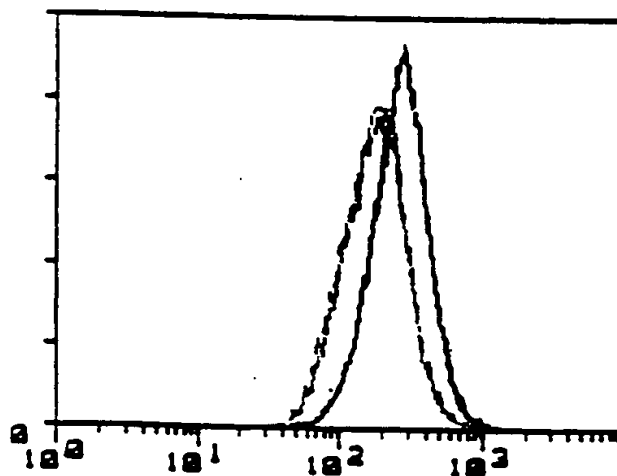
FIGURE 23

A



—————	0 ng anti-Tac
.....	10 ng
-----	20 ng
- . - . -	40 ng

B



—————	0 ng anti-Tac
.....	20 ng anti-Tac
-----	20 ng humanized anti-Tac

FIGURE 24



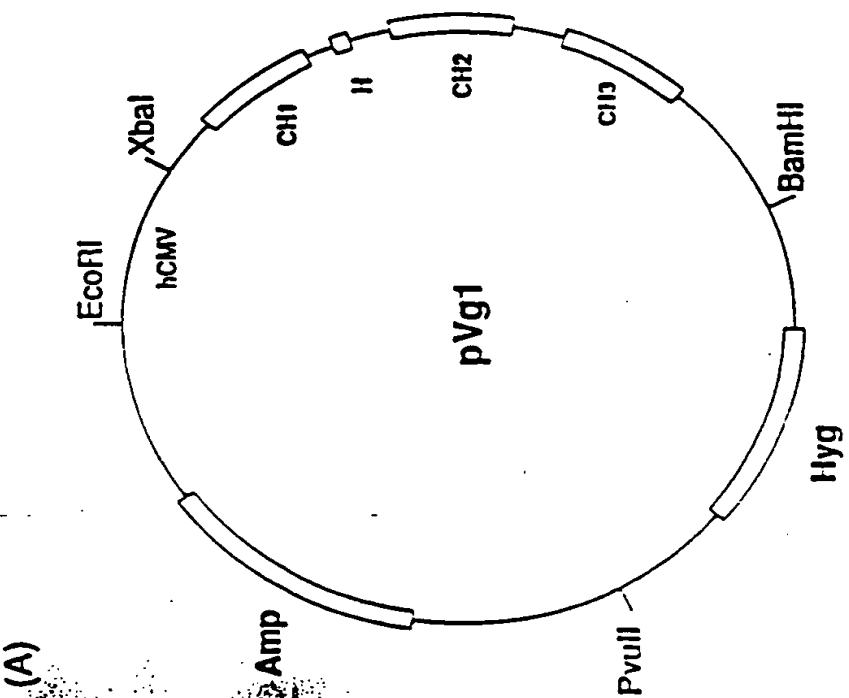
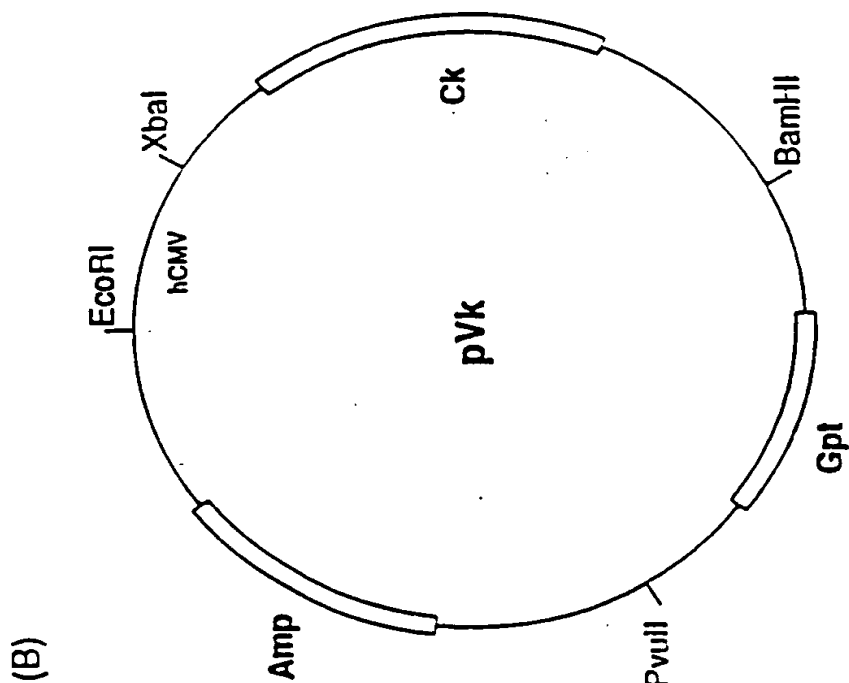


FIGURE 25

07 634278

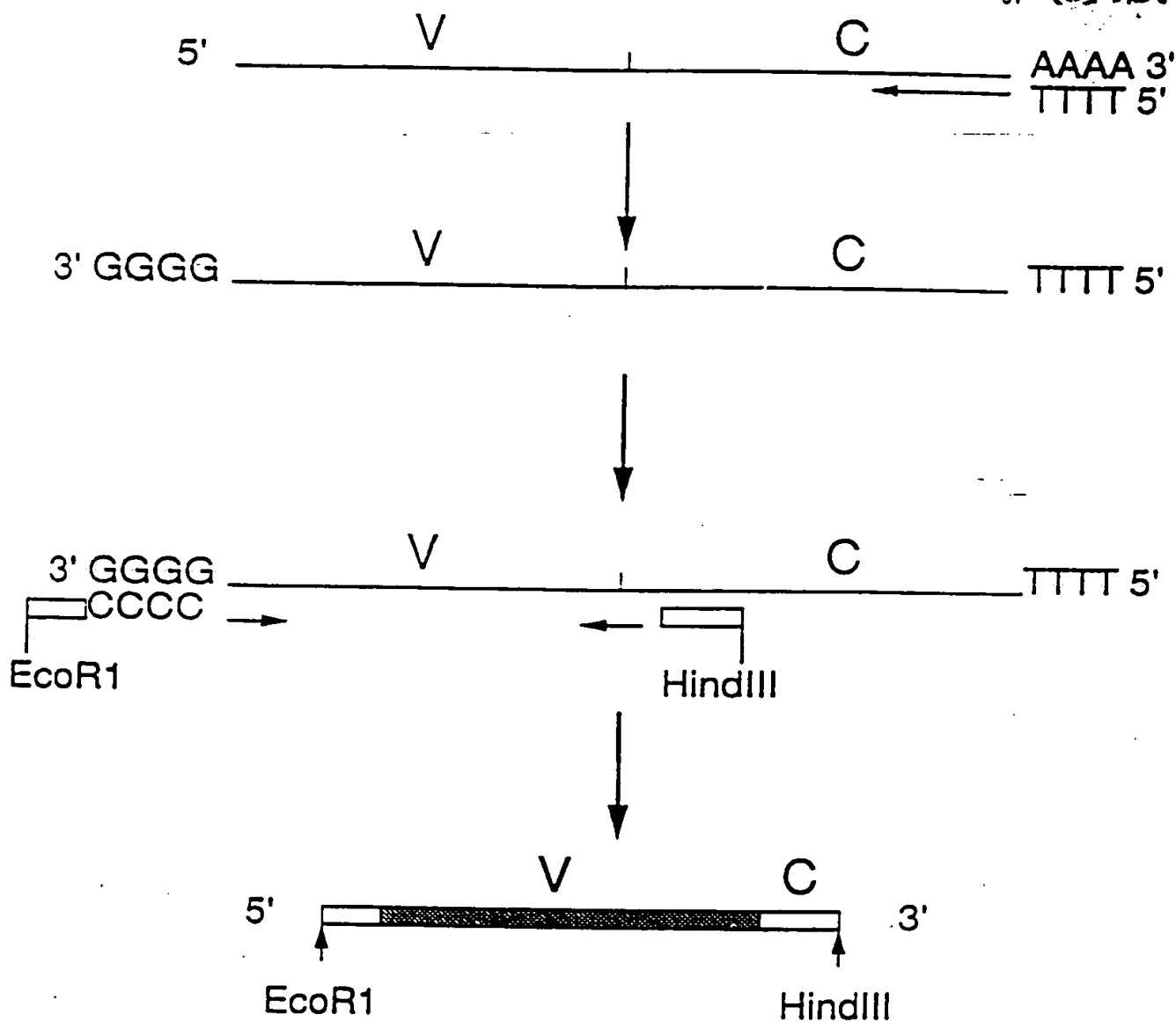


FIGURE 26

A

07-634278

30 60  
 ATGGATTTTCAAGTGCAGATTTTCAGCTTCCTGCTAATCAGTGCCTCAGTCATACTGTCC  
 M D F Q V Q I F S F L L I S A S V I L S

90 120  
 AGAGGACAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCTGCGTCTCCAGGGGAGAAG  
 R G Q I V L T Q S P A I M S A S P G E K

150 180  
 GTCACCATGACCTGCAGTGGCAGCTCAAGTGTAAGTTTCATGTACTGGTACCAGCAGAGG  
 V T M T C S G S S S V S F M Y W Y Q Q R

210 240  
 CCAGGATCCTCCCCAGACTCCTGATTTATGACACATCCAACCTGGCTTCTGGAGTCCCT  
 P G S S P R L L I Y D T S N L A S G V P

270 300  
 GTTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCCGAATGGAG  
 V R F S G S G S G T S Y S L T I S R M E

330 360  
 GCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTACTTACCCGCTCAGGTTEGGT  
 A E D A A T Y Y C Q Q W S T Y P L T F G

GCTGGGACCAAGCTGGAGCTGAAA  
 A G T K L E L K

B

30 60  
 ATGGCTGTCTTGGGGCTGCTCTTCTGCCTGGTGACATTCCCAAGCTGTGTCTATCCCAG  
 M A V L G L L F C L V T F P S C V L S Q

90 120  
 GTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC  
 V Q L K Q S G P G L V Q P S Q S L S I T

150 180  
 TGCACAGTCTCTGGTTTCTCAGTAACAAGTTATGGTGTACACTGGATTCCGCCAGTCTCCA  
 C T V S G F S V T S Y G V H W I R Q S P

210 240  
 GGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGTGGTGAAGCACAGACTATAATGCA  
 G K G L E W L G V I W S G G S T D Y N A

270 300  
 GCTTTCATATCCAGACTGACCATCAGCAAGGACAACTCCAAGAGCCAAGTTTCTTTAAA  
 A F I S R L T I S K D N S K S Q V F F K

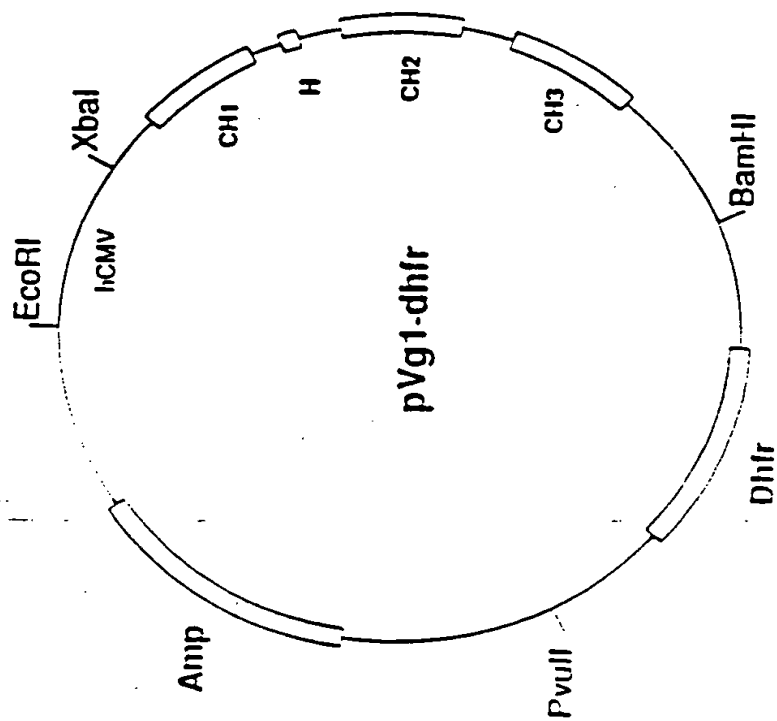
330 360  
 GTGAACAGTCTGCAACCTGCTGACACAGCCATATACTATTGTGCCAGAGCTGGGGACTAT  
 V N S L Q P A D T A I Y Y C A R A G D Y

390  
 AATTACGACGGTTTGTCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCG  
 N Y D G F A Y W G Q G T L V T V S A

FIGURE 27

07 63427

(A)



(B)

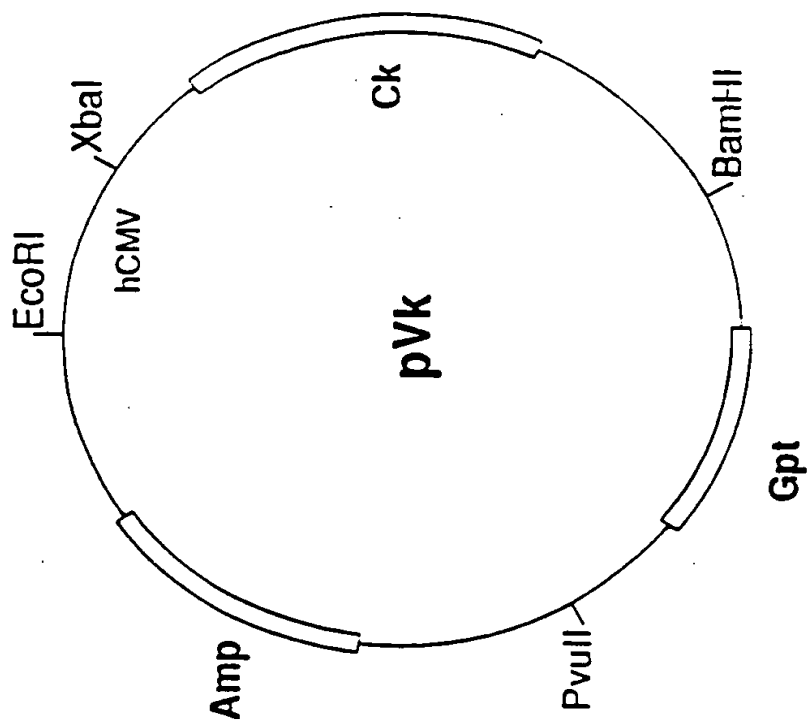


FIGURE 28



01 634278

A

1	D	I	Q	M	T	Q	S	P	S	S	L	S	V	S	V	G	D	R	V	T
1	D	I	Q	M	T	Q	S	P	S	S	L	S	<u>A</u>	S	V	G	D	R	V	T
21	I	T	C	Q	A	S	Q	N	V	N	A	Y	L	N	W	Y	Q	Q	K	P
21	I	T	C	<u>S</u>	<u>G</u>	<u>S</u>	<u>S</u>	<u>S</u>	<u>V</u>		<u>S</u>	<u>F</u>	<u>M</u>	<u>Y</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>	<u>P</u>
41	G	L	A	P	K	L	L	I	Y	G	A	S	T	R	E	A	G	V	P	S
40	G	<u>K</u>	A	P	K	L	L	I	Y	<u>D</u>	<u>T</u>	<u>S</u>	<u>N</u>	<u>L</u>	<u>A</u>	<u>S</u>	G	V	P	S
61	R	F	S	G	S	G	S	G	T	D	<u>F</u>	T	F	T	I	S	S	L	Q	P
60	R	F	S	G	S	G	S	G	T	D	<u>Y</u>	T	F	T	I	S	S	L	Q	P
81	E	D	I	A	T	Y	Y	C	Q	Q	Y	N	N	W	P	P	T	F	G	Q
80	E	D	I	A	T	Y	Y	C	<u>Q</u>	<u>Q</u>	<u>W</u>	<u>S</u>	<u>T</u>	<u>Y</u>	<u>P</u>	<u>L</u>	<u>T</u>	<u>F</u>	<u>G</u>	<u>Q</u>
101	G	T	K	V	E	V	K													
100	G	T	K	V	E	V	K													

B

1	A	V	Q	L	L	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L
1	<u>E</u>	V	Q	L	L	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L
21	S	C	A	A	S	G	F	T	F	S	A	S	A	M	S	W	V	R	Q	A
21	S	C	A	A	S	G	F	T	<u>V</u>	<u>T</u>	<u>S</u>	<u>Y</u>	<u>G</u>	<u>V</u>	<u>H</u>	<u>W</u>	<u>V</u>	<u>R</u>	<u>Q</u>	<u>A</u>
41	P	G	K	G	L	E	W	V	A	W	K	Y	E	N	G	N	D	K	H	Y
41	P	G	K	G	L	E	W	V	<u>G</u>		<u>V</u>	<u>I</u>	<u>W</u>	<u>S</u>	<u>G</u>	<u>G</u>	<u>S</u>	<u>T</u>	<u>D</u>	<u>Y</u>
61	A	D	S	V	N	G	R	F	T	I	S	R	N	D	S	K	N	T	L	Y
60	<u>N</u>	<u>A</u>	<u>A</u>	<u>F</u>	<u>I</u>	<u>S</u>	<u>R</u>	<u>F</u>	<u>T</u>	<u>I</u>	<u>S</u>	<u>R</u>	<u>D</u>	<u>N</u>	<u>S</u>	<u>K</u>	<u>N</u>	<u>T</u>	<u>L</u>	<u>Y</u>
81	L	Q	M	N	G	L	Q	A	Z	V	S	A	I	Y	Y	C	A	R	D	A
80	L	Q	M	N	<u>S</u>	L	Q	A	E	<u>D</u>	<u>T</u>	A	I	Y	Y	C	A	R	<u>A</u>	
101	G	P	Y	V	S	P	T	F	F	A	H	W	G	Q	G	T	L	V	T	V
99	<u>G</u>	<u>D</u>	<u>Y</u>		<u>N</u>	<u>Y</u>	<u>D</u>	<u>G</u>	<u>F</u>	<u>A</u>	<u>Y</u>	<u>W</u>	<u>G</u>	<u>Q</u>	<u>G</u>	<u>T</u>	<u>L</u>	<u>V</u>	<u>T</u>	<u>V</u>
121	S	S																		
118	S	S																		

FIGURE 30

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VC13

10 20 30 40 50 60  
 TTCTGCTGGT ACCAGTACAT GAAACTTACA CTTGAGCTGC CACTGCAGGT GATGGTGACG  
 70 80 90 100  
 TGGTCACCCA CTGAGGCACT GAGGCTAGAT GGAGACTGGG TCATTTG

VC14

10 20 30 40 50 60  
 CATGTACTGG TACCAGCAGA AGCCAGGAAA AGCTCCGAAA CTTCTGATTT ATGACACATC  
 70 80 90 100 110 120  
 CAACCTGGCT TCTGGAGTCC CTTCCCGCTT CAGTGGCAGT GGGTCTGGGA CCGATTACAC  
 130  
 CTTTACAATC TCTTCA

VC15

10 20 30 40 50 60  
 TGTGTCTAGA AAAGTGTACT TACGTTTTAC CTCGACCTTG GTCCCTTGAC CGAACGTGAG  
 70 80 90 100 110 120  
 CGGGTAAGTA CTCCACTGCT GGCAGTAATA AGTGGCTATA TCTTCCGGCT GAAGTGAAGA  
 130  
 GATTGTAAAG GTGTAAT

VC16

10 20 30 40 50 60  
 CACATCTAGA CCACCATGGA TTTTCAAGTG CAGATCTTCA GCTTCCTGCT AATCAGTGCC  
 70 80 90 100  
 TCAGTCATAC TGTCCAGAGG AGATATTCAA ATGACCCAGT CTCCATCT

FIGURE 31A

07 634278

vc11

10 20 30 40 50 60  
TAGTCTGTCG ACCCACCCT CCATATCACT CCCACCCACT CGAGTCCCTT TCCAGGAGCC  
70 80 90 100 110 120  
TGGCGGACCC AGTGTACACC ATAACCTGTT ACGGTGAAAC CACTGGCGGC ACAAGACAGT  
130  
CTCAGAGATC CTCCTGGC

vc12

10 20 30 40 50 60  
TGGTGGGTCG ACAGACTATA ATGCAGCTTT CATATCCAGA TTTACCATCA GCAGAGACAA  
70 80 90 100 110 120  
CAGCAAGAAC AACTGTATC TCCAAATGAA TAGCCTGCAA GCCGAGGACA CAGCCATATA  
TTATTG

wps54

10 20 30 40 50 60  
AACTCTAGA CCACCATGGC TGTCTTGGGG CTGCTCTTCT GCCTGGTGAC ATTCCCAAGC  
70 80 90 100 110 120  
TGTGTCCTAT CCGCTGTCCA GCTGCTAGAG AGTGGTGGCG GTCTGGTGCA GCCAGGAGGA  
130  
TCTCTGAGAC

wps57

10 20 30 40 50 60  
AACTCTAGA AGTTAGGACT CACCTGAAGA GACAGTGACC AGAGTCCCTT GGCCCCAGTA  
70 80 90 100 110  
AGCAAAACCG TCGTAATTAT AGTCCCCAGC TCTGGCACAA TAATATATGG CTGTGTCC

FIGURE 31B



07 634278

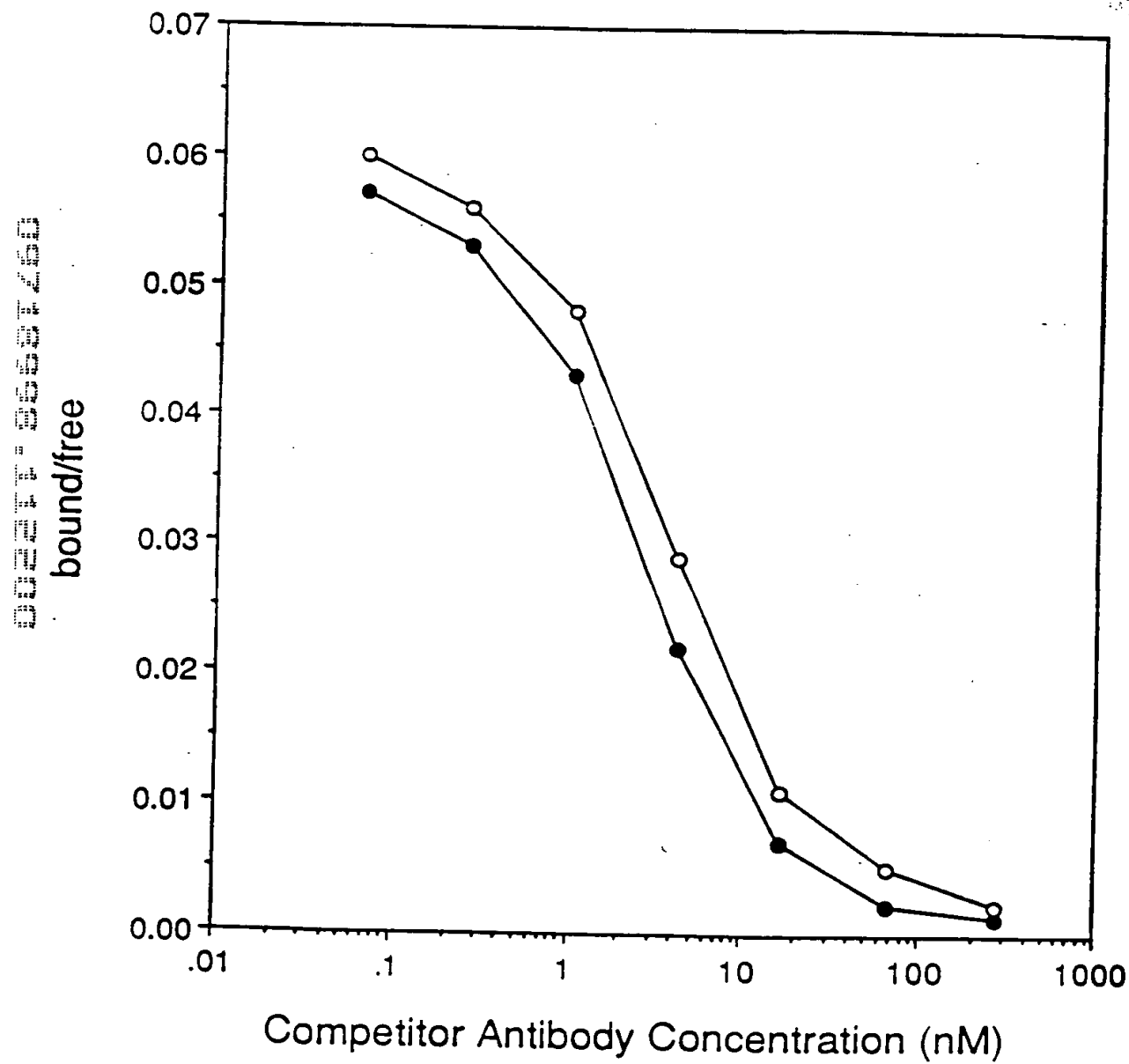


FIGURE 32

07 634278

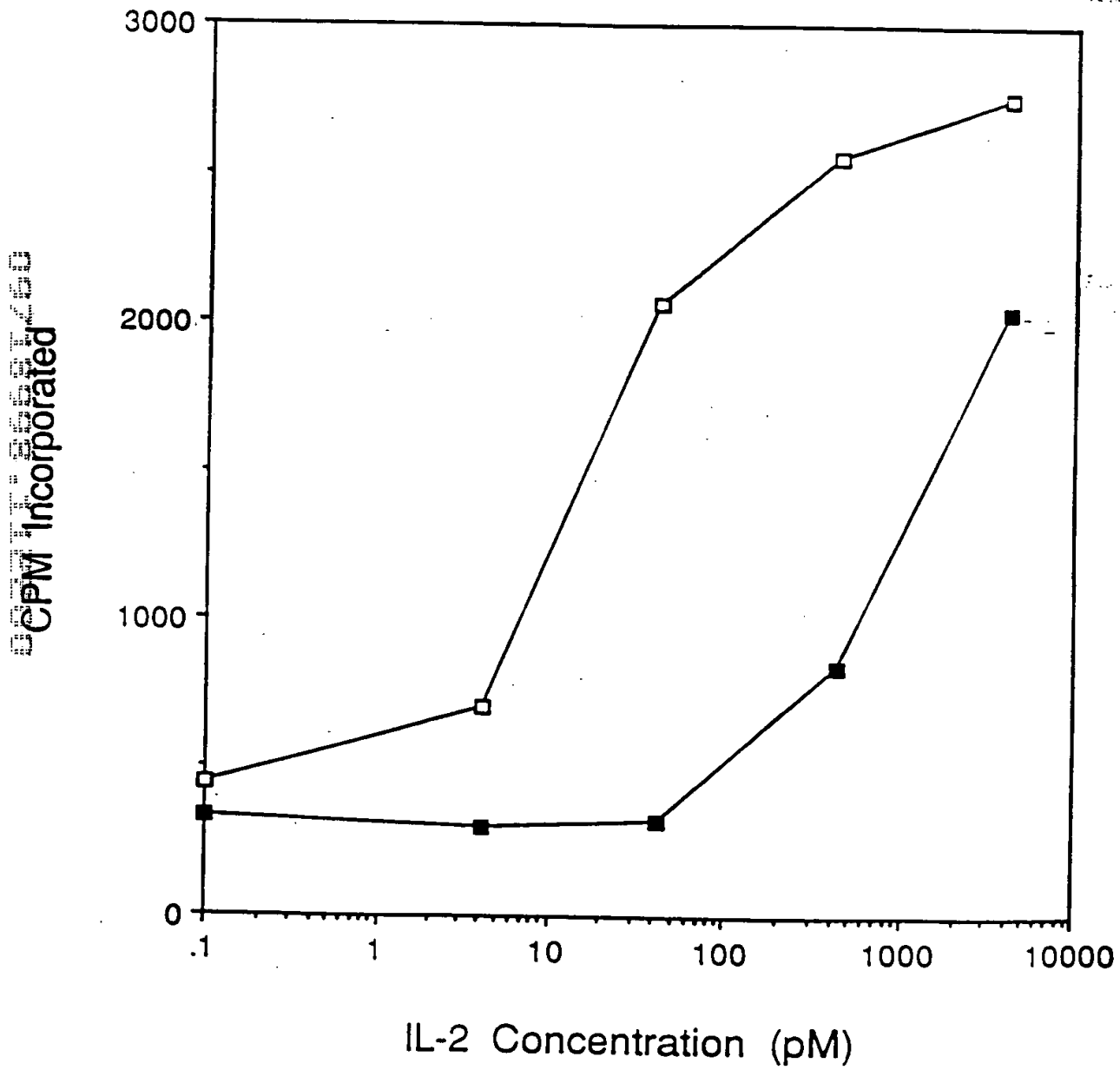


FIGURE 33

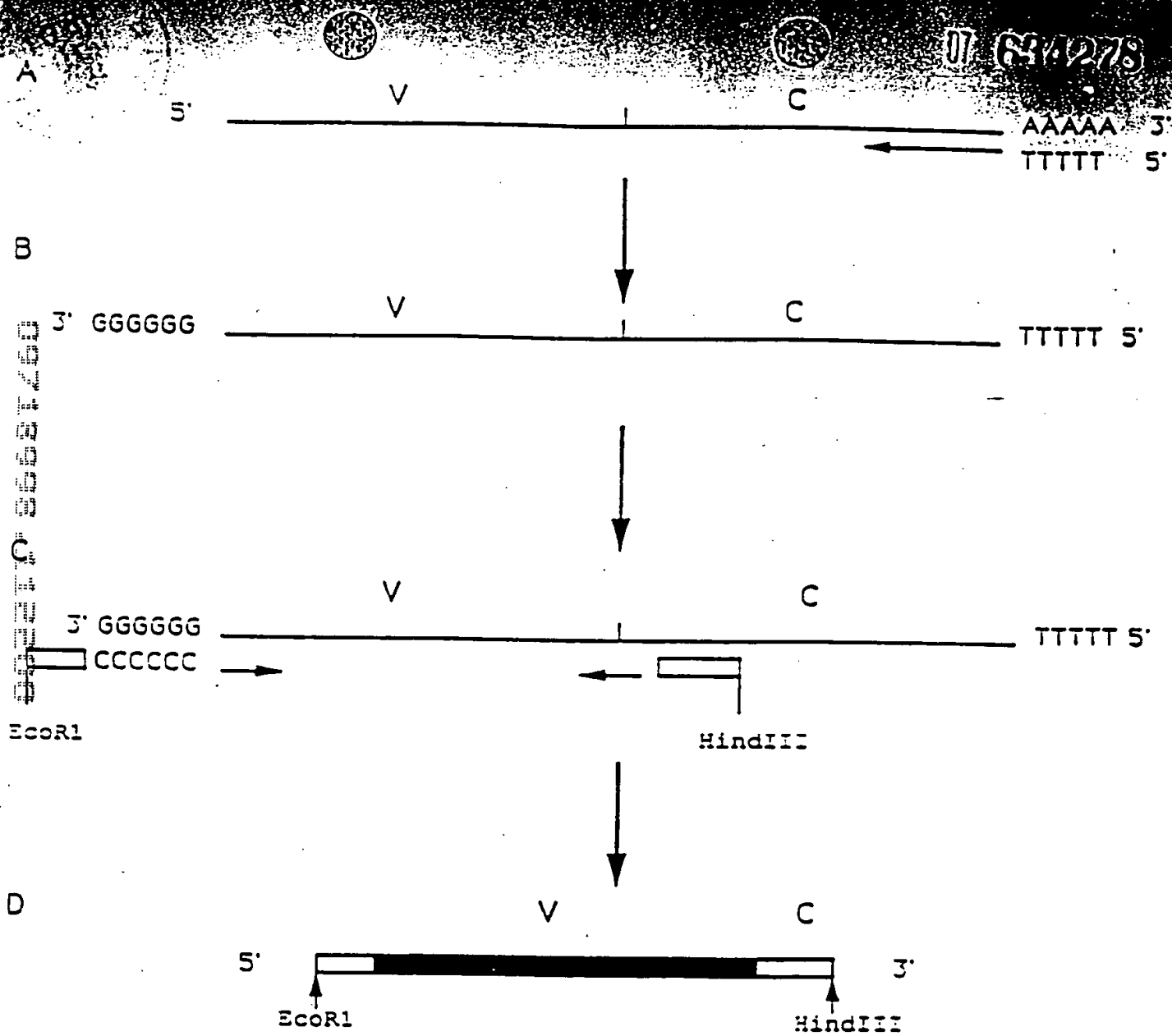


FIGURE 34

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SCANNED # 14

(A)

1	5	10	15	20
E M I L V E S G G L V K P G A S L K L				
E V Q L L E S G G L V Q P G S L R L				
25	30	35	40	
S C A A S G F T F S N Y G L S W V R Q T				
S C A A S G F T F S N Y G L S W V R Q A				
45	50	52	55	
S D R R L E W V A S I S R G G R I Y S				
P G K G L E W V A S I S R G G R I Y S				
60	65	70	75	
P D N L K G R F T I S R E D A K N T L Y				
P D N L K G R F T I S R E D A K N T L Y				
80	82	85	90	95
L Q M S S L K S E D T A L Y Y C L R E G				
L Q M S S L K S E D T A L Y Y C L R E G				
100	102	105	110	
I Y Y A D Y G F F D V W G T G T T V I V				
I Y Y A D Y G F F D V W G T G T T V I V				
113				
S S				
S S				

FIGURE 35A

(B)

[illegible]

**FIGURE 35B**

(C)

1	5	10	15	20
Q V Q L Q Q S D A E L V K K P G A S V K I				
Q V Q L V Q S G A E E V K K P G S S V K V				
25	30	35	40	
S C K V S G Y T F T D H T I H W M K Q R				
S C K A S G Y T F T D H T I H W M R Q A				
45	50	52 a	55	
P E Q G L E W F G Y I Y P R D G H T R Y				
P G Q G L E W F G Y I Y P R D G H T R Y				
60	65	70	75	
S E K F K G K A T L T A D K S A S T A Y				
A E K F K G K A T I T A D E S T N T A Y				
80	82 a	85	90	95
M H L N S L T S E D S A V Y F C A R G R				
M E L S S L R S E D T A V Y F C A R G R				
100 a	b	c	d	105
D S R E R N G F A Y W G Q G T L V T V S				
D S R E R N G F A Y W G Q G T L V T V S				
113				
A				
S				

FIGURE 35C

(D)

1	5	10	15	20
D I V M T Q S H K F M S T S V G D R V S				
D I Q M T Q S P S T L S A S V G D R V T				
25	30	35	40	
I T C K A S Q D V G S A V V W H Q Q K S				
I T C K A S Q D V G S A V V W H Q Q K P				
45	50	55	60	
G Q S P K L L I Y W A S T R H T G V P D				
G K A P K L L I Y W A S T R H T G V P S				
65	70	75	80	
R F T G S G S G T D F T L T I T N V Q S				
R F T G S G S G T E F T L T I S S L Q P				
85	90	95	100	
E D L A D Y F C Q Q Y S I F P L T F G A				
D D F A T Y F C Q Q Y S I F P L T F G Q				
105	107			
G T R L E L K				
G T K V E V K				

FIGURE 35D

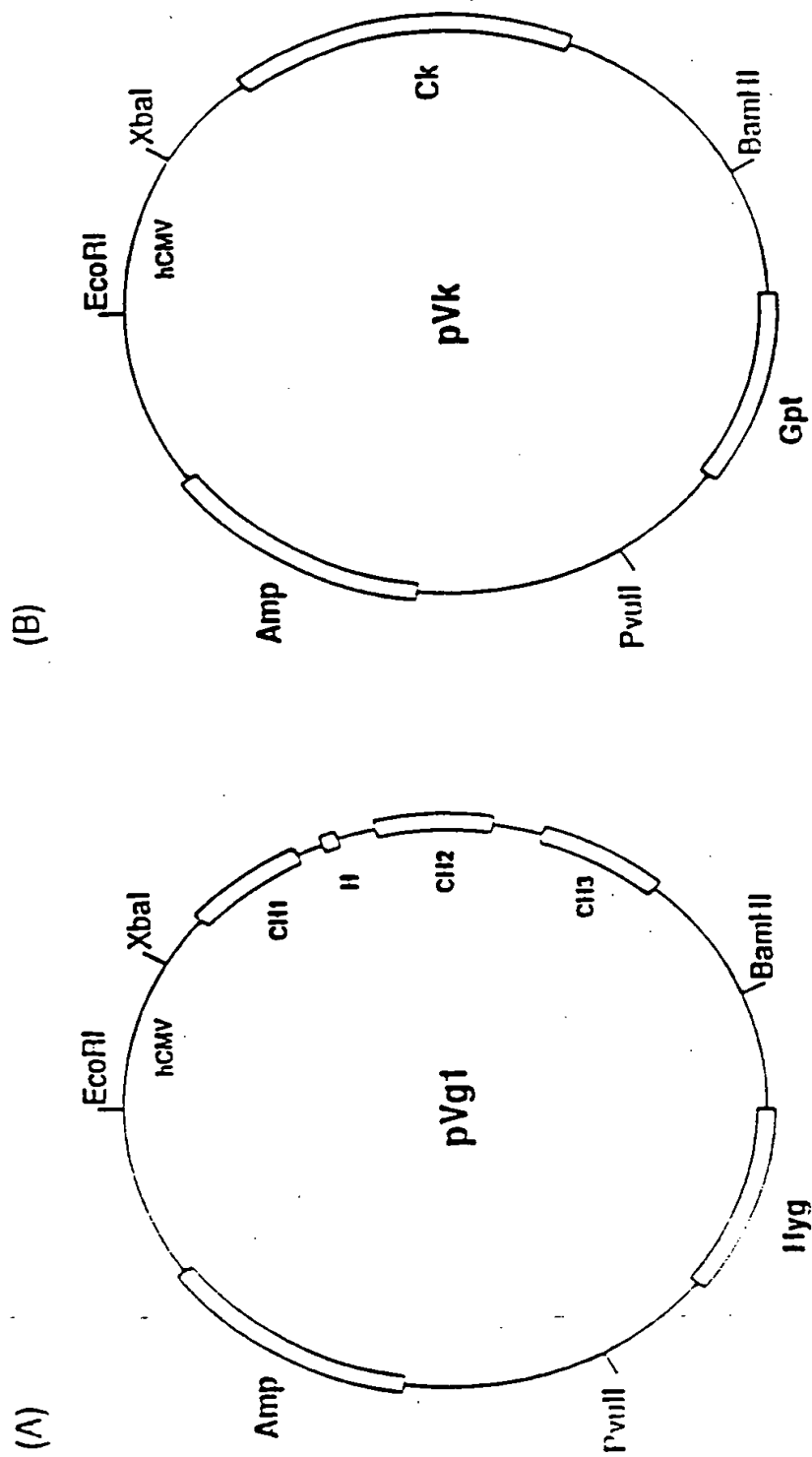


FIGURE 36



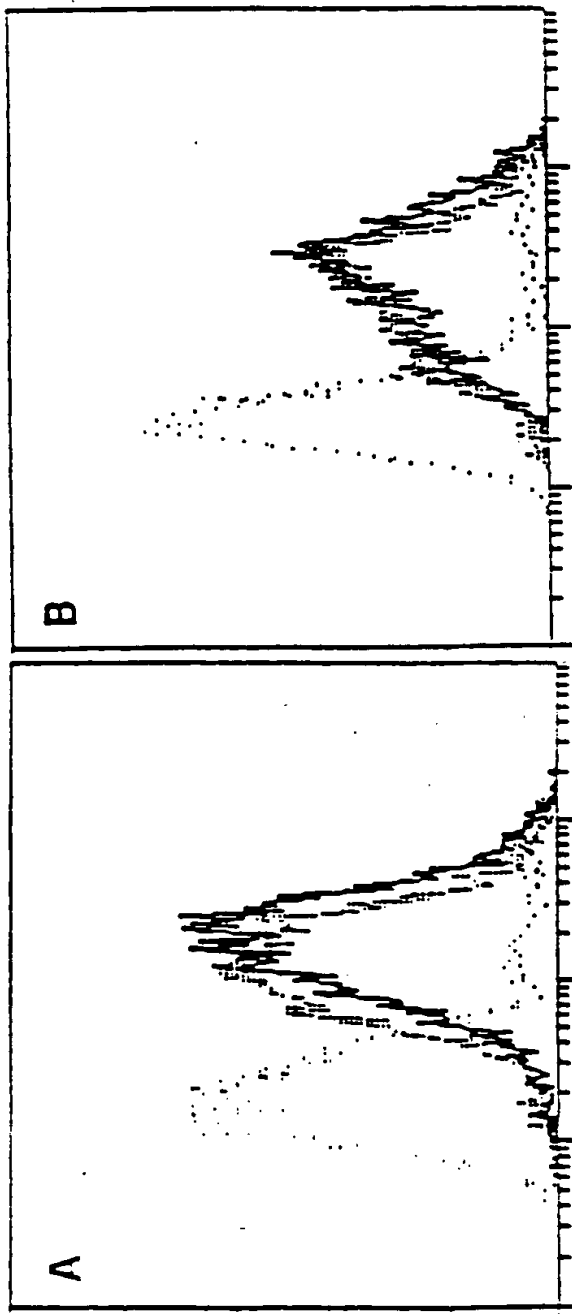


FIGURE 37

(A)

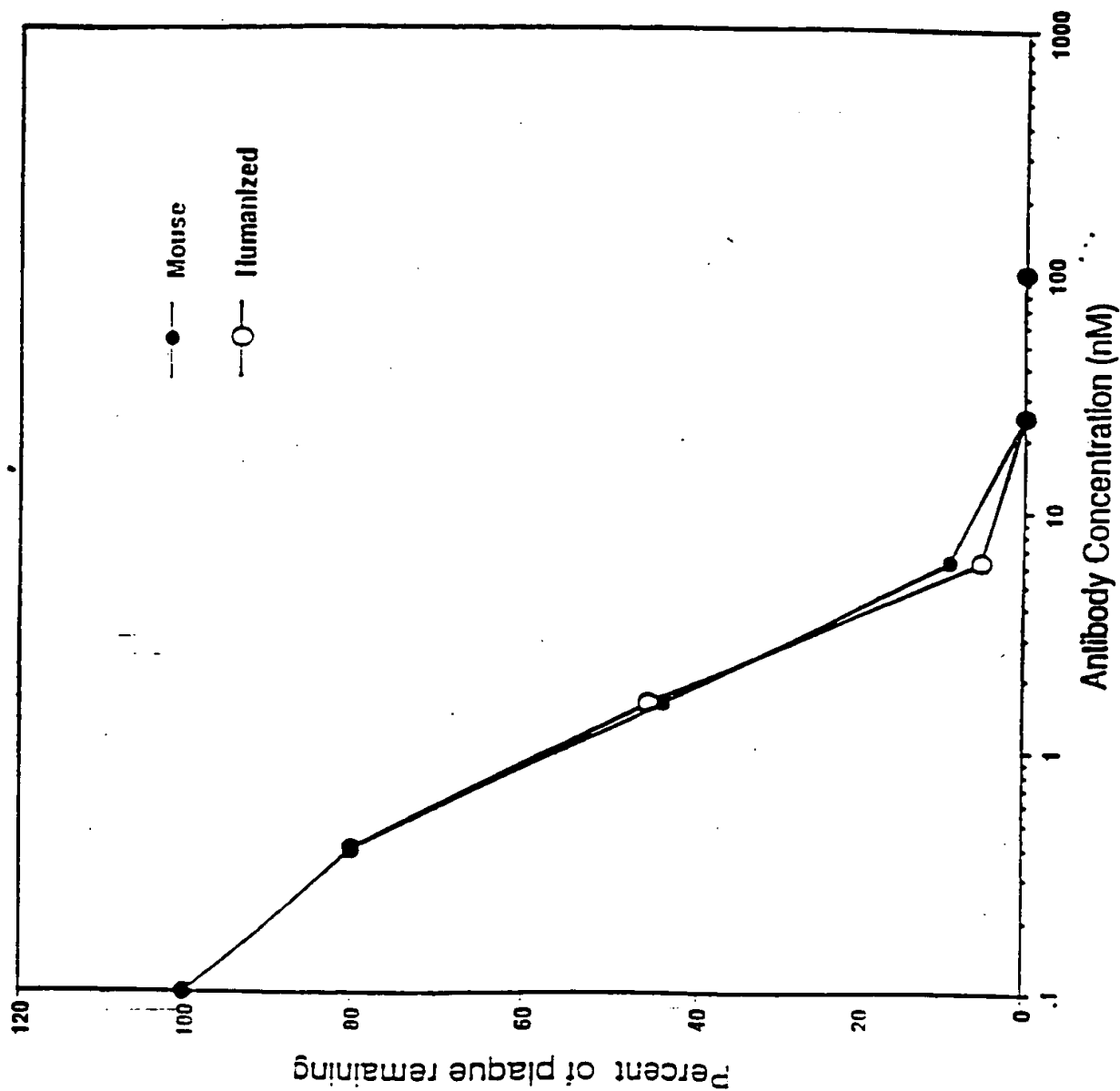


FIGURE 38A

SCANNED, # 14

(B)

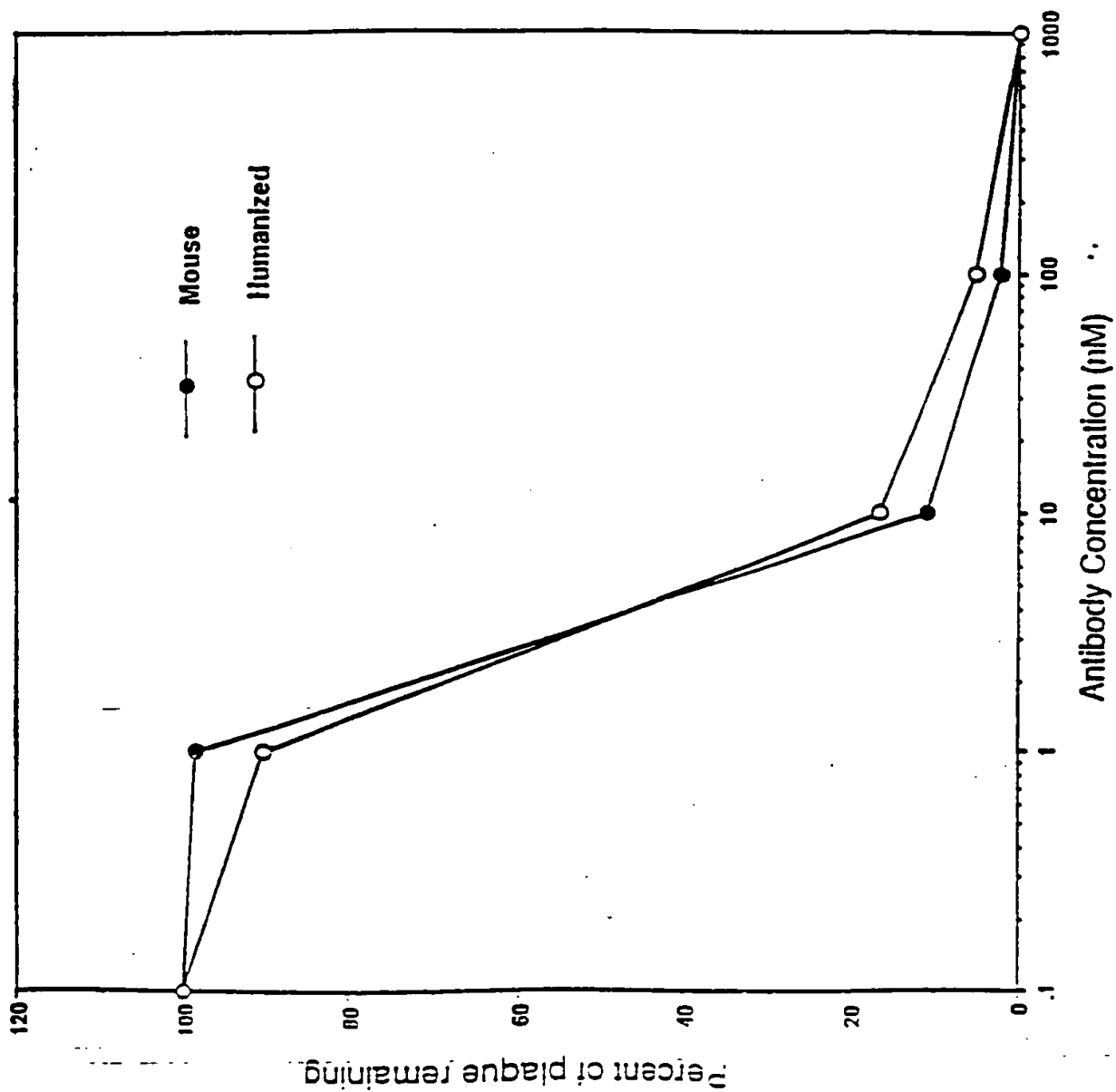
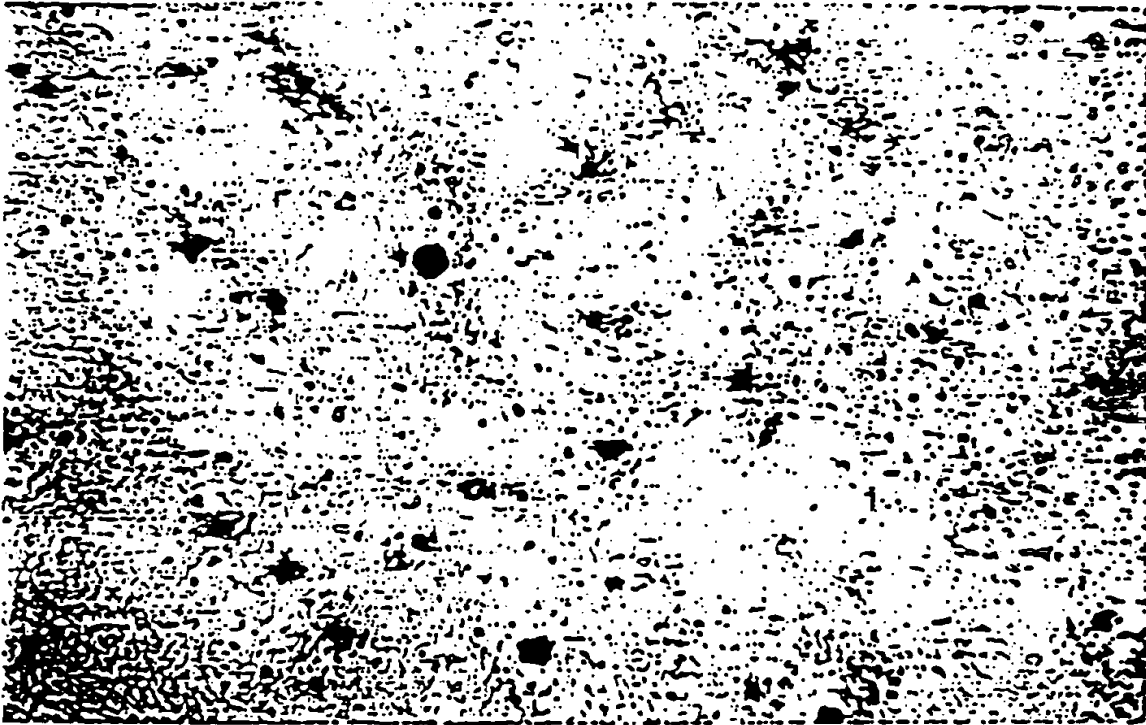


FIGURE 38B

(A)

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(B)

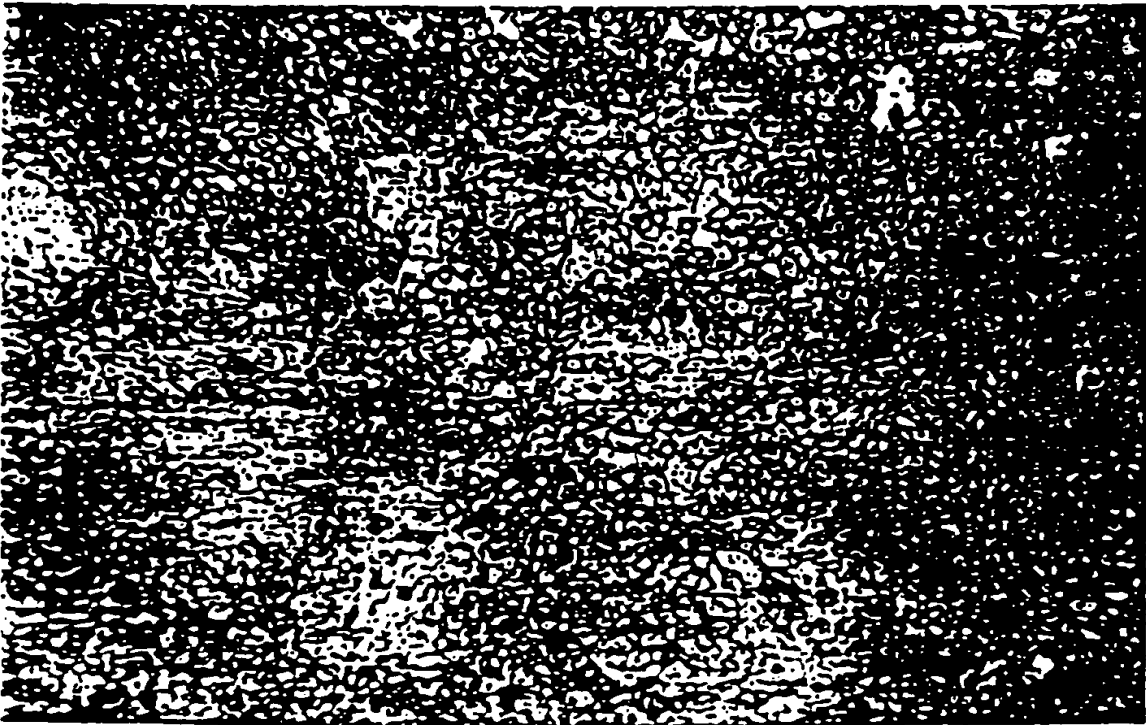


FIGURE 39

The diagram illustrates the construction of a recombinant plasmid. It starts with a linear DNA fragment containing a variable region (V) and constant regions (C). This fragment is ligated into a circular plasmid vector (pUC19) which has a multiple cloning site (MCS) with HindIII and EcoRI sites. The resulting recombinant plasmid is then digested with HindIII and EcoRI to produce a linear DNA fragment for electroporation into *E. coli* cells.

**FIGURE 40**

A

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30 60  
 ATGGAGAAAGACACACTCCTGCTATGGGTCCTGCTTCTCTGGGTTCCAGGTTCCACAGGT  
 M E K D T L L L W V L L L W V P G S T G

90 120  
 GACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGGCCACC  
 D I V L T Q S P A S L A V S L G Q R A T

150 180  
 ATCTCCTGCAGAGCCAGCGAAAGTGTGATAATTATGGCATTAGTTTATGAAGTGGTTC  
 I S C R A S E S V D N Y G I S F M N W F

210 240  
 CAACAGAAACCAGGACAGCCACCCAACTCCTCATCTATGCTGCATCCAACCAAGGATCC  
 Q Q K P G Q P P K L L I Y A A S N Q G S

270 300  
 GGGGTCCCTGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCAGCCTCAACATCCAT  
 G V P A R F S G S G S G T D F S L N I H

330 360  
 CCTATGGAGGAGGATGATACTGCAATGTATTTCTGTGTCAGCAAAGTAAGGAGGTTCCGTGG  
 P M E E D D T A M Y F C Q Q S K E V P W

390  
 ACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA  
 T F G G G T K L E I K

B

30 60  
 ATGGGATGGAGCTGGATCTTTCTCTTCCTCCTGTCAGGAACCTGCAGGCGTCCACTCTGAG  
 M G W S W I F L F L L S G T A G V H S E

90 120  
 GTCCAGCTTCAGCAGTCAGGACCTGAGCTGGTGAAACCTGGGGCCTCAGTGAAGATATCC  
 V Q L Q Q S G P E L V K P G A S V K I S

150 180  
 TGCAAGGCTTCTGGATACACATTCAGTACTACAACATGCACTGGGTGAAGCAGAGCCAT  
 C K A S G Y T F T D Y N M H W V K Q S H

210 240  
 GGAAAGAGCCTTGAGTGGATTGGATATATTTATCCTTACAATGGTGGTACTGGCTACAAC  
 G K S L E W I G Y I Y P Y N G G T G Y N

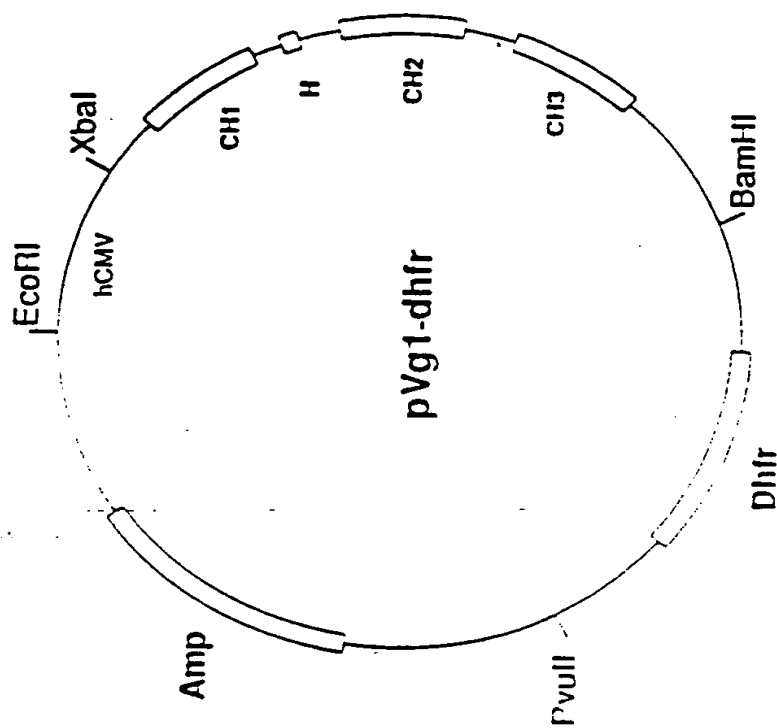
270 300  
 CAGAAGTTCAAGAGCAAGGCCACATTGACTGTAGACAATTCCTCCAGCACAGCCTACATG  
 Q K F K S K A T L T V D N S S S T A Y M

330 360  
 GACGTCCGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGAGGGCGCCCC  
 D V R S L T S E D S A V Y Y C A R G R P

390  
 GCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA  
 A M D Y W G Q G T S V T V S S

FIGURE 41

(A)



(B)

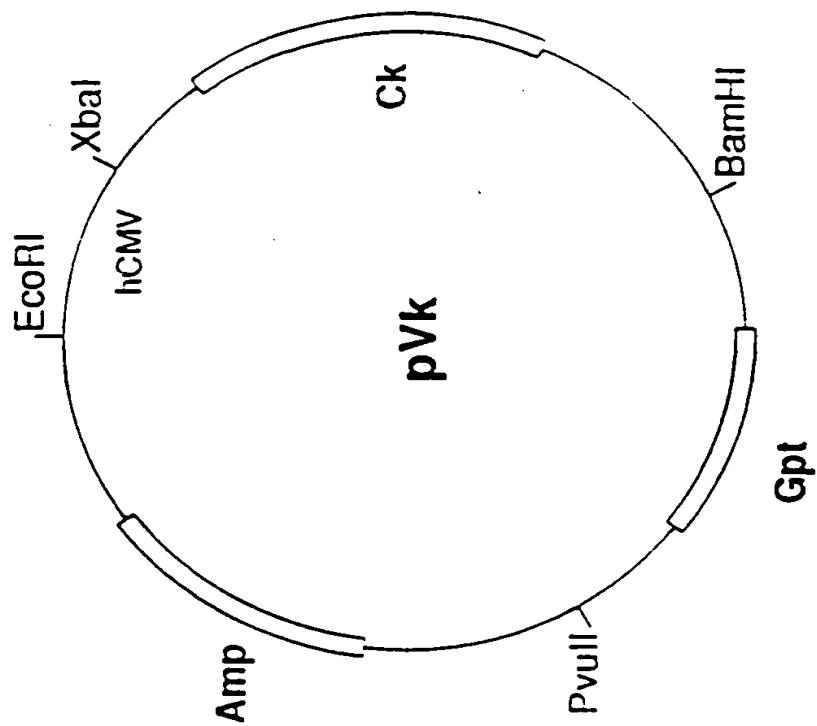
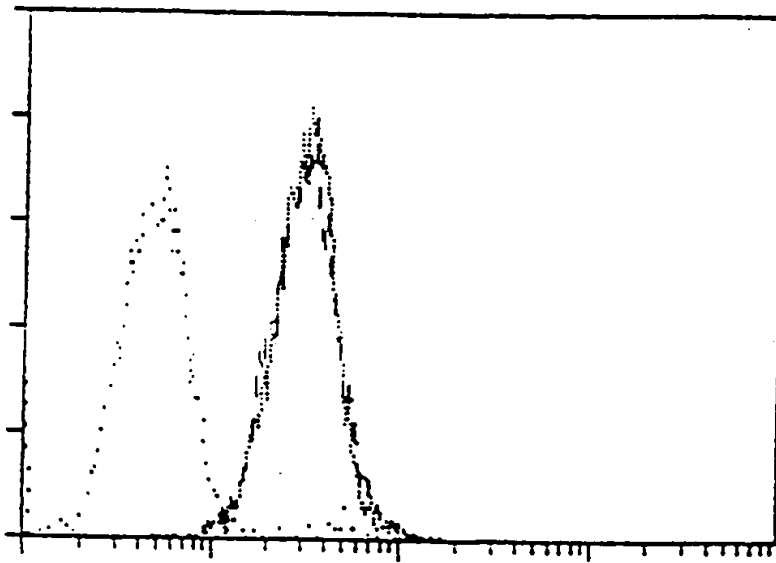


FIGURE 42

[illegible]

22



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A

1	D	I	Q	M	T	Q	S	P	S	<u>T</u>	L	S	A	S	V	G	D	R	V	T
1	D	I	Q	M	T	Q	S	P	S	<u>S</u>	L	S	A	S	V	G	D	R	V	T
21	I	T	C	R	A	S	Q	S		I	N				T	W	L	A	W	Y
21	I	T	C	<u>R</u>	<u>A</u>	<u>S</u>	<u>E</u>	<u>S</u>	<u>V</u>	<u>D</u>	<u>N</u>	<u>Y</u>	<u>G</u>	<u>I</u>	<u>S</u>	<u>F</u>	<u>M</u>	<u>N</u>	<u>W</u>	<u>P</u>
37	Q	Q	K	P	G	K	A	P	K	L	L	M	Y	K	A	S	S	L	E	S
41	Q	Q	K	P	G	K	A	P	K	L	L	<u>I</u>	Y	<u>A</u>	<u>A</u>	<u>S</u>	<u>N</u>	<u>Q</u>	<u>G</u>	<u>S</u>
57	G	V	P	S	R	F	<u>I</u>	G	S	G	S	G	T	<u>E</u>	<u>F</u>	<u>T</u>	<u>L</u>	<u>T</u>	<u>I</u>	<u>S</u>
61	G	V	P	S	R	F	<u>S</u>	G	S	G	S	G	T	<u>D</u>	<u>F</u>	<u>T</u>	<u>L</u>	<u>T</u>	<u>I</u>	<u>S</u>
77	S	L	Q	P	D	D	F	A	T	Y	Y	C	Q	Q	Y	N	S	D	S	K
81	S	L	Q	P	D	D	F	A	T	Y	Y	C	<u>Q</u>	<u>Q</u>	<u>S</u>	<u>K</u>	<u>E</u>	<u>V</u>	<u>P</u>	<u>W</u>
97	M	F	G	Q	G	T	K	V	E	V	K									
101	<u>T</u>	F	G	Q	G	T	K	V	E	<u>I</u>	K									

B

1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V
1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V
21	S	C	K	A	S	G	<u>G</u>	T	F	<u>S</u>	R	S	A	I	I	W	V	R	Q	A
21	S	C	K	A	S	G	<u>Y</u>	T	F	<u>T</u>	<u>D</u>	<u>Y</u>	<u>N</u>	<u>M</u>	<u>H</u>	<u>W</u>	<u>V</u>	<u>R</u>	<u>Q</u>	<u>A</u>
41	P	G	Q	G	L	E	W	M	G	<u>G</u>	<u>I</u>	<u>V</u>	<u>P</u>	<u>M</u>	<u>F</u>	<u>G</u>	<u>P</u>	<u>P</u>	<u>N</u>	<u>Y</u>
41	P	G	Q	G	L	E	W	<u>I</u>	G	<u>Y</u>	<u>I</u>	<u>Y</u>	<u>P</u>	<u>Y</u>	<u>N</u>	<u>G</u>	<u>G</u>	<u>T</u>	<u>G</u>	<u>Y</u>
61	A	Q	K	F	Q	G	R	V	T	I	T	A	D	E	S	T	N	T	A	Y
61	<u>N</u>	<u>Q</u>	<u>K</u>	<u>F</u>	<u>K</u>	<u>S</u>	<u>K</u>	<u>A</u>	<u>T</u>	<u>I</u>	<u>T</u>	<u>A</u>	<u>D</u>	<u>E</u>	<u>S</u>	<u>T</u>	<u>N</u>	<u>T</u>	<u>A</u>	<u>Y</u>
81	M	E	L	S	S	L	R	S	E	D	T	A	<u>F</u>	<u>Y</u>	<u>F</u>	<u>C</u>	<u>A</u>	<u>G</u>	<u>G</u>	<u>Y</u>
81	M	E	L	S	S	L	R	S	E	D	T	A	<u>V</u>	<u>Y</u>	<u>Y</u>	<u>C</u>	<u>A</u>	<u>R</u>	<u>G</u>	
101	G	I	Y	S	P	E	E	Y	N	G	G	L	V	T	V	S	S			
100	<u>R</u>	<u>P</u>	<u>A</u>	<u>M</u>	<u>D</u>	<u>Y</u>	<u>W</u>	<u>G</u>	<u>Q</u>	<u>G</u>	<u>T</u>	<u>L</u>	<u>V</u>	<u>T</u>	<u>V</u>	<u>S</u>	<u>S</u>			

FIGURE 44

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ma1

10 20 30 40 50 60  
 TATATCTAGA CCACCATGGG ATGGAGCTGG ATCTTTCTCT TCCTCCTGTC AGGAACTGCT  
 70 80 90 100 110 120  
 GCGTCCACT CTCAGGTTCA GCTGGTGCAG TCTGGAGCTG AGGTGAAGAA GCCTGGGAGC  
 130  
 TCAGTGAAGG TT

ma2

10 20 30 40 50 60  
 AGCCGGTACC ACCATTGTAA GGATAAATAT ATCCAATCCA TTCCAGGCCT TGGCCAGGAG  
 70 80 90 100 110 120  
 CCTGCCTCAC CCAGTGCATG TTGTAGTCAG TGAAGGTGTA GCCAGAAGCT TTGCAGGAAA  
 130  
 CCTTCACTGA GCT

ma3

10 20 30 40 50 60  
 TGGTGGTACC GGCTACAACC AGAAGTTCAA GAGCAAGGCC ACAATTACAG CAGACGAGAG  
 70 80 90 100 110  
 TACTAACACA GCCTACATGG AACTCTCCAG CCTGAGGTCT GAGGACACTG CA

ma4

10 20 30 40 50 60  
 TATATCTAGA GGCCATTCTT ACCTGAAGAG ACAGTGACCA GAGTCCCTTG GCCCCAGTAG  
 70 80 90 100 110  
 TCCATAGCGG GCGGCCCTCT TGCGCAGTAA TAGACTGCAG TGTCTCAGA C

FIGURE 45A

634278

ma5

10	20	30	40	50	60
TATATCTAGA	CCACCATGGA	GAAAGACACA	CTCCTGCTAT	GGGTCCTGCT	TCTCTGGGTT
70	80	90	100	110	120
CCAGGTTCCA	CAGGTGACAT	TCAGATGACC	CAGTCTCCGA	GCTCTCTGTC	CGCATCAGTA

GG

ma6

10	20	30	40	50	60
TCAGAAGCTT	AGGAGCCTTC	CCGGGTTTCT	GTTGGAACCA	G TTCATAAAG	CTAATGCCAT
70	80	90	100	110	120
AATTGTCGAC	ACTTTCGCTG	GCTCTGCATG	TGATGGTGAC	CCTGTCTCCT	ACTGATGCCG

AC

ma7

10	20	30	40	50	60
TCCTAAGCTT	CTGATTTACG	CTGCATCCAA	CCAAGGCTCC	GGGGTACCCT	CTCGCTTCTC
70	80	90	100	110	
AGGCAGTGGA	TCTGGGACAG	ACTTCACTCT	CACCATTTC	TCTCTGCAGC	CTGATGACT

ma8

10	20	30	40	50	60
TATATCTAGA	CTTTGGATTTC	TACTTACGTT	TGATCTCCAC	CTTGGTCCCT	TGACCGAACG
70	80	90	100	110	
TCCACGGAAC	CTCCTTACTT	TGCTGACAGT	AATAGGTTGC	GAAGTCATCA	GGCTGCAG

FIGURE 45B

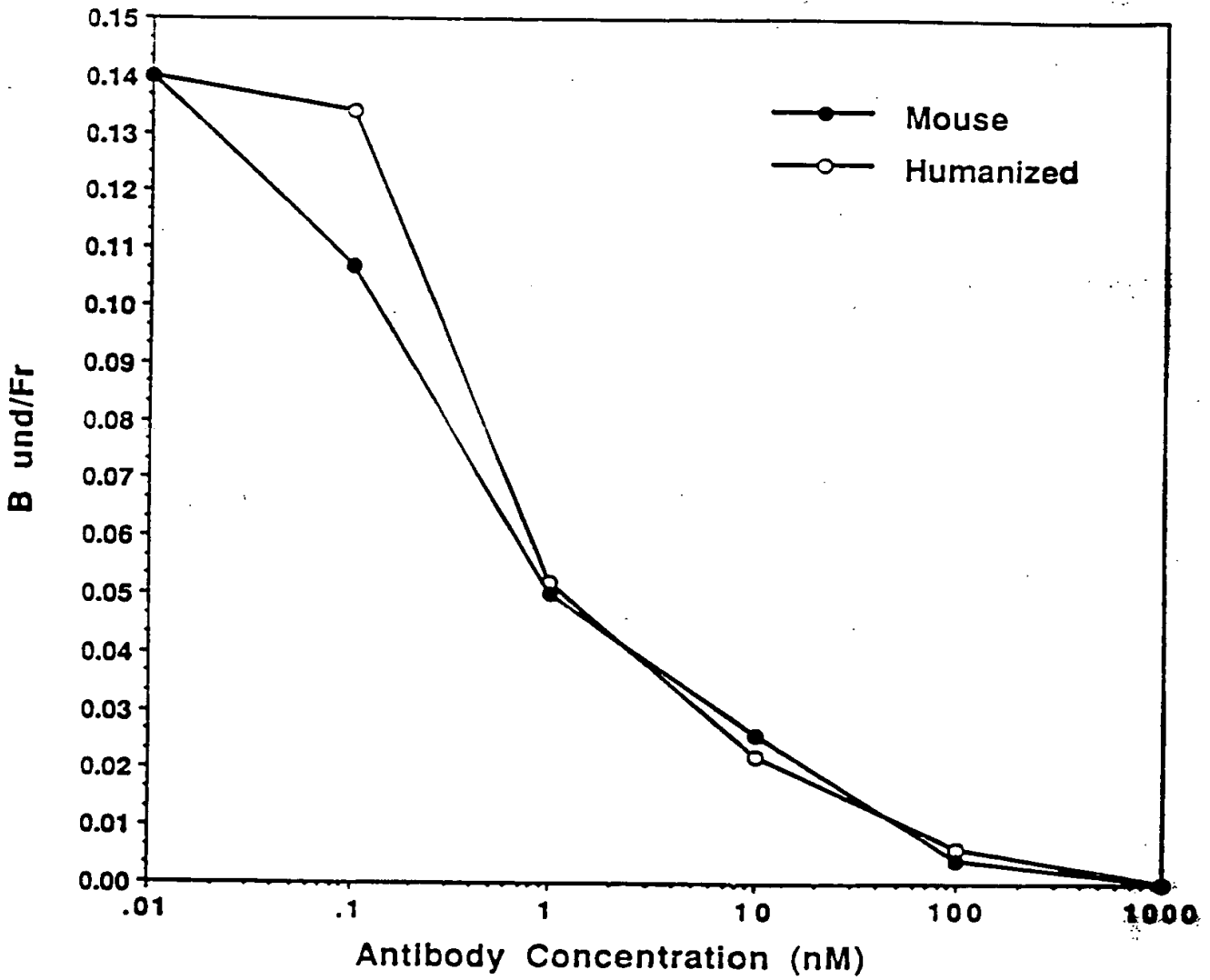


FIGURE 46

07 634278

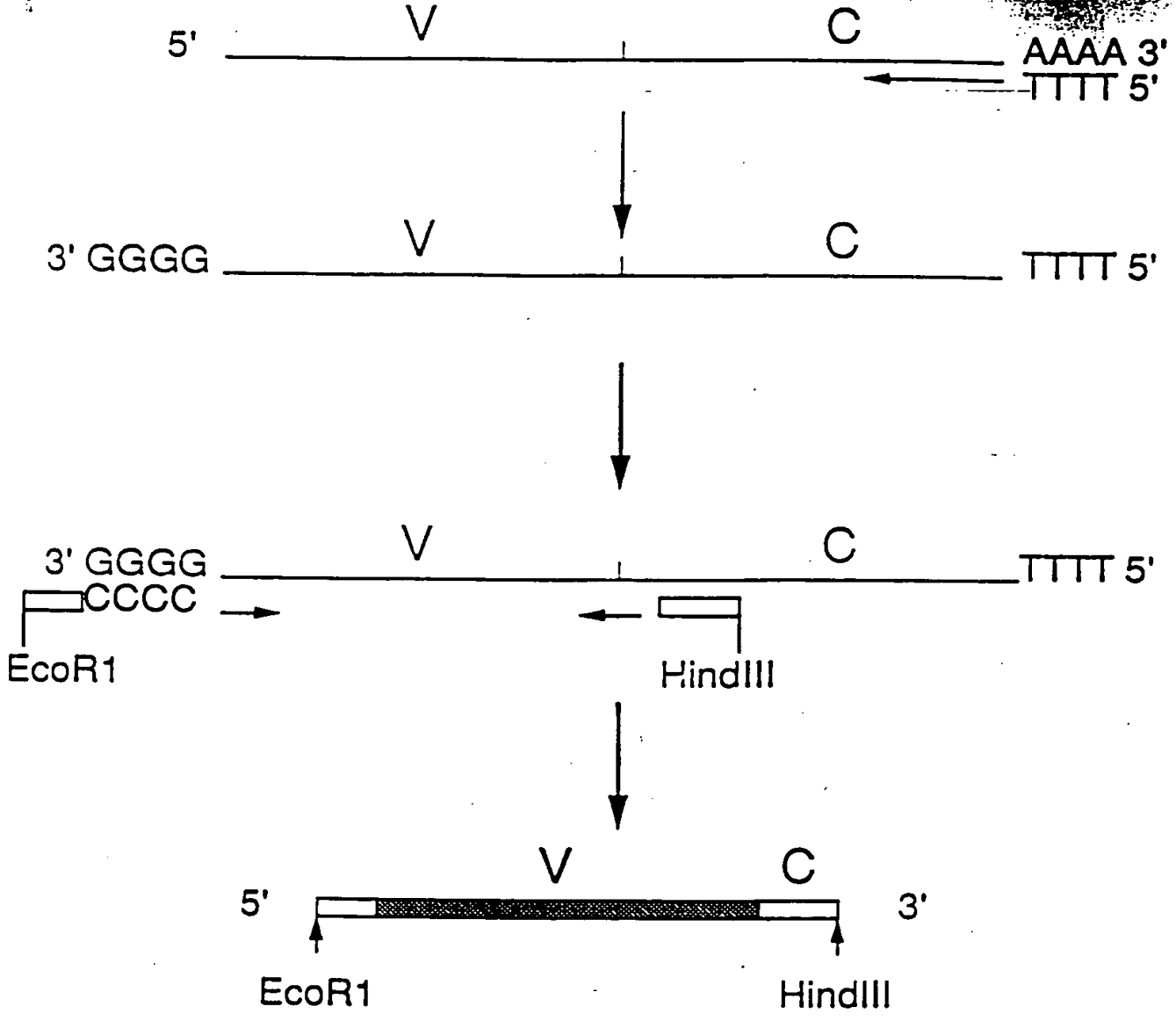


FIGURE 47

A

07 634278

30 60  
ATGGTTTTCACACCTCAGATACTTGGACTTATGCTTTTTTGGATTTCAGCCTCCAGAGGT  
M V F T P Q I L G L M L F W I S A S R G

↓ 90 120  
GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACTCCGGGAGATAGCGTCAGT  
D I V L T Q S P A T L S V T P G D S V S

150 180  
CTTTCCTGCAGGGCCAGCCAAAGTATTAGCAACAACCTACACTGGTATCAACAAAATCA  
L S C R A S Q S I S N N L H W Y Q Q K S

210 240  
CATGAGTCTCCAAGGCTTCTCATCAAGTATGCTTCCCAGTCCATCTCTGGGATCCCCCTCC  
H E S P R L L I K Y A S Q S I S G I P S

270 300  
AGGTTTCAGTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTGTCAACGGTGTGGAGACT  
R F S G S G S G T D F T L S V N G V E T

330 360  
GAAGATTTTGAATGTATTTCTGTCAACAGAGTAACAGTTGGCCTCATACGTTTCGGAGGG  
E D F G M Y F C Q Q S N S W P H T F G G

GGGACCAAGCTGGAAATAAAA  
G T K L E I K

B

30 60  
ATGGGATGGAGCTGGATCTTTCTCTTCTCCTGTCAGGAAGTGCAGGTGTCCACTCTGAG  
M G W S W I F L F L L S G T A G V H S E

90 120  
GTCCAGCTGCAACAGTCTGGACCTGAGCTGGTGAAGCCTGGAGCTTCAATGAAGATATCC  
V Q L Q Q S G P E L V K P G A S M K I S

150 180  
TGCAAGGCTTCTGTTTACTCATTCACTGGCTACACCATGAACTGGGTGAAGCAGAGCCAT  
C K A S V Y S F T G Y T M N W V K Q S H

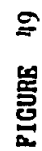
210 240  
GGACAGAACCTTGAGTGGATTGGACTTATTAATCCTTACAATGGTGGTACTAGCTACAAC  
G Q N L E W I G L I N P Y N G G T S Y N

270 300  
CAGAAGTTCAAGGGGAAGGCCACATTAAGTGTAGACAAGTCATCCAACACAGCCTACATG  
Q K F K G K A T L T V D K S S N T A Y M

330 360  
GAGCTCCTCAGTCTGACATCTGCGGACTCTGCAGTCTATTACTGTACAAGACGGGGGTTT  
E L L S L T S A D S A V Y Y C T R R G F

390  
CGAGACTATTCTATGGACTACTGGGGTCAAGGAACTCAGTCACCGTCTCCTCA  
R D Y S M D Y W G Q G T S V T V S S

FIGURE 48



07 634278

A

1	E	I	V	L	T	Q	S	P	G	T	L	S	L	S	P	G	E	R	A	T
1	E	I	V	L	T	Q	S	P	G	T	L	S	L	S	P	G	E	R	A	T
21	L	S	C	R	A	S	Q	S	V	S	S	G	Y	L	G	N	Y	Q	Q	K
21	L	S	C	R	A	S	Q	S		I	S	N	N	L	H	N	Y	Q	Q	K
41	P	G	Q	A	P	R	L	L	I	Y	G	A	S	S	R	A	T	G	I	P
40	P	G	Q	A	P	R	L	L	I	<u>K</u>	<u>Y</u>	<u>A</u>	<u>S</u>	<u>Q</u>	<u>S</u>	<u>I</u>	<u>S</u>	G	I	P
61	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	R	L	E
60	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	R	L	E
81	P	E	D	F	A	V	Y	Y	C	Q	Q	Y	G	S	L	G	R	T	F	G
80	P	E	D	F	A	V	Y	Y	C	<u>Q</u>	<u>Q</u>	<u>S</u>	<u>N</u>	<u>S</u>	<u>W</u>	<u>P</u>	<u>H</u>	<u>T</u>	<u>F</u>	<u>G</u>
101	Q	G	T	K	V	E	I	K												
100	Q	G	T	K	V	E	I	K												

B

1	Q	V	Q	L	M	Q	S	G	A	E	V	K	K	P	G	S	S	V	R	V
1	Q	V	Q	L	<u>V</u>	Q	S	G	A	E	V	K	K	P	G	S	S	V	R	V
21	S	C	K	T	S	G	G	T	F	V	D	Y	K	G	L	W	V	R	Q	A
21	S	C	K	<u>A</u>	S	G	<u>Y</u>	<u>S</u>	<u>F</u>	<u>T</u>	<u>G</u>	<u>Y</u>	<u>T</u>	<u>M</u>	<u>N</u>	<u>W</u>	<u>V</u>	<u>R</u>	<u>Q</u>	<u>A</u>
41	P	G	K	G	L	E	W	V	G	Q	I	P	L	R	F	N	G	E	V	K
41	P	G	K	G	L	E	W	V	G	<u>L</u>	<u>I</u>	<u>N</u>	<u>P</u>	<u>Y</u>	<u>N</u>	<u>G</u>	<u>G</u>	<u>T</u>	<u>S</u>	<u>Y</u>
61	N	P	G	S	V	V	R	V	S	V	S	L	K	P	S	F	N	Q	A	N
61	<u>N</u>	<u>Q</u>	<u>K</u>	<u>F</u>	<u>K</u>	<u>G</u>	<u>R</u>	<u>V</u>	<u>T</u>	<u>V</u>	<u>S</u>	<u>L</u>	<u>K</u>	<u>P</u>	<u>S</u>	<u>F</u>	<u>N</u>	<u>Q</u>	<u>A</u>	<u>Y</u>
81	M	E	L	S	S	L	F	S	E	D	T	A	V	Y	Y	C	A	R	E	Y
81	M	E	L	S	S	L	F	S	E	D	T	A	V	Y	Y	C	<u>T</u>	<u>R</u>	<u>R</u>	
101	G	F	D	T	S	D	Y	Y	Y	Y	Y	W	G	Q	G	T	L	V	T	V
100	<u>G</u>	<u>F</u>			<u>R</u>	<u>D</u>	<u>Y</u>	<u>S</u>	<u>M</u>	<u>D</u>	<u>Y</u>	<u>W</u>	<u>G</u>	<u>Q</u>	<u>G</u>	<u>T</u>	<u>L</u>	<u>V</u>	<u>T</u>	<u>V</u>
121	S	S																		
118	S	S																		

FIGURE 50



07 634278

jb16

10	20	30	40	50	60
TAGATCTAGA	CCACCATGGT	TTTCACACCT	CAGATACTAG	GACTCATGCT	CTTCTGGATT
70	80	90	100	110	120
TCAGCCTCCA	GAGGTGAAAT	TGTGCTAACT	CAGTCTCCAG	GCACCCTAAG	CTTATCACCG

GGAGAAAGG

jb17

10	20	30	40	50	60
TAGACAGAAT	TCACGCGTAC	TTGATAAGTA	GACGTGGAGC	TTGTCCAGGT	TTTGTTGGT
70	80	90	100	110	120
ACCAGTGTAG	GTTGTTGCTA	ATACTTTGGC	TGGCCCTGCA	GGAAAGTGTA	GCCCTTTCTC

CCGGTGAT

jb18

10	20	30	40	50	60
AAGAGAATTC	ACGCGTCCCA	GTCCATCTCT	GGAATACCCG	ATAGGTTTCAG	TGGCAGTGGA
70	80	90	100	110	
TCAGGGACAG	ATTTCACTCT	CACAATAAGT	AGGCTCGAGC	CGGAAGATTT	TGC

jb19

10	20	30	40	50	60
TAGATCTAGA	GTTGAGAAGA	CTACTTACGT	TTTATTTCTA	CCTTGGTCCC	TTGTCCGAAC
70	80	90	100	110	
GTATGAGGCC	AACTGTTACT	CTGTTGACAA	TAATACACAG	CAAAATCTTC	CGGCTC

FIGURE 51A

07 634278

jb20

10	20	30	40	50	60
TATATCTAGA	CCACCATGGG	ATGGAGCTGG	ATCTTTCTCT	TCCTCCTGTC	AGGAACTGCA
70	80	90	100	110	120
GGTGTCCACT	CTCAAGTCCA	ACTGGTACAG	TCTGGAGCTG	AGGTAAAAA	GCCTGGAAGT
130					
TCAGTAAGAG	TTTC				

jb21

10	20	30	40	50	60
TATATAGGTA	CCACCATGTG	AAGGATTAAT	AAGTCCAACC	CACTCAAGTC	CTTTTCCAGG
70	80	90	100	110	120
TGCCTGTCTC	ACCCAGTTCA	TGGTATACCC	AGTGAATGAG	TATCCGGAAG	CTTTGCAGGA
130					
AACTCTTACT	GAAC				

jb22

10	20	30	40	50	60
TATATAGGTA	CCAGCTACAA	CCAGAAGTTC	AAGGGCAGAG	TTACAGTTTC	TTTGAAGCCT
70	80	90	100	110	
TCATTTAACC	AGGCCTACAT	GGAGCTCAGT	AGTCTGTTTT	CTGAAGACAC	TGCAGT

jb23

10	20	30	40	50	60
TATATCTAGA	GGCCATTCTT	ACCTGAGGAG	ACGGTGACTA	AGGTTCCCTG	ACCCAGTAG
70	80	90	100	110	
TCCATAGAAT	AGTCTCGAAA	CCCCCGTCTT	GTACAGTAAT	AGACTGCAGT	GTCTTC

FIGURE 51B

07 634278

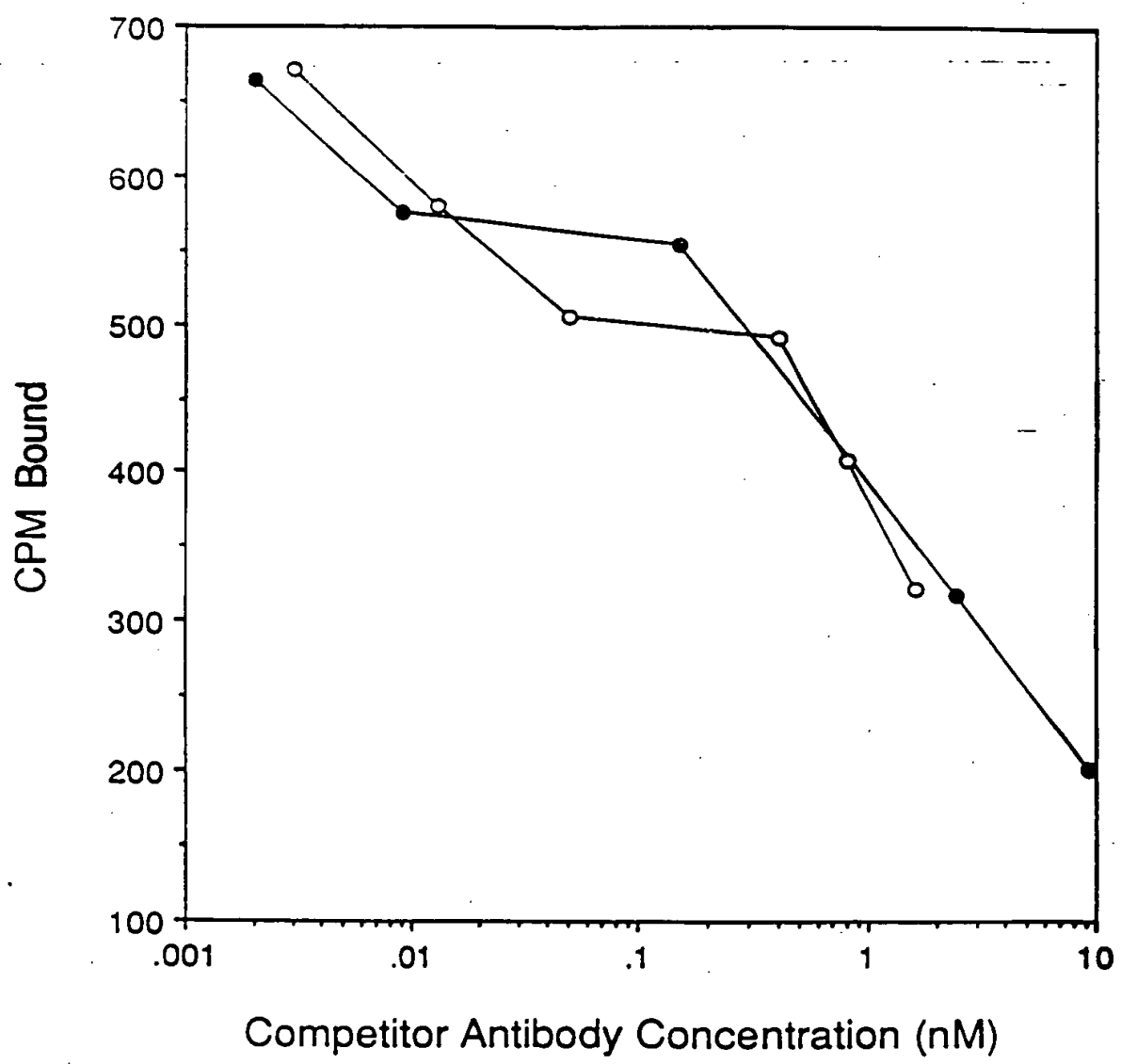


FIGURE 52

07 634278

007405000 112200

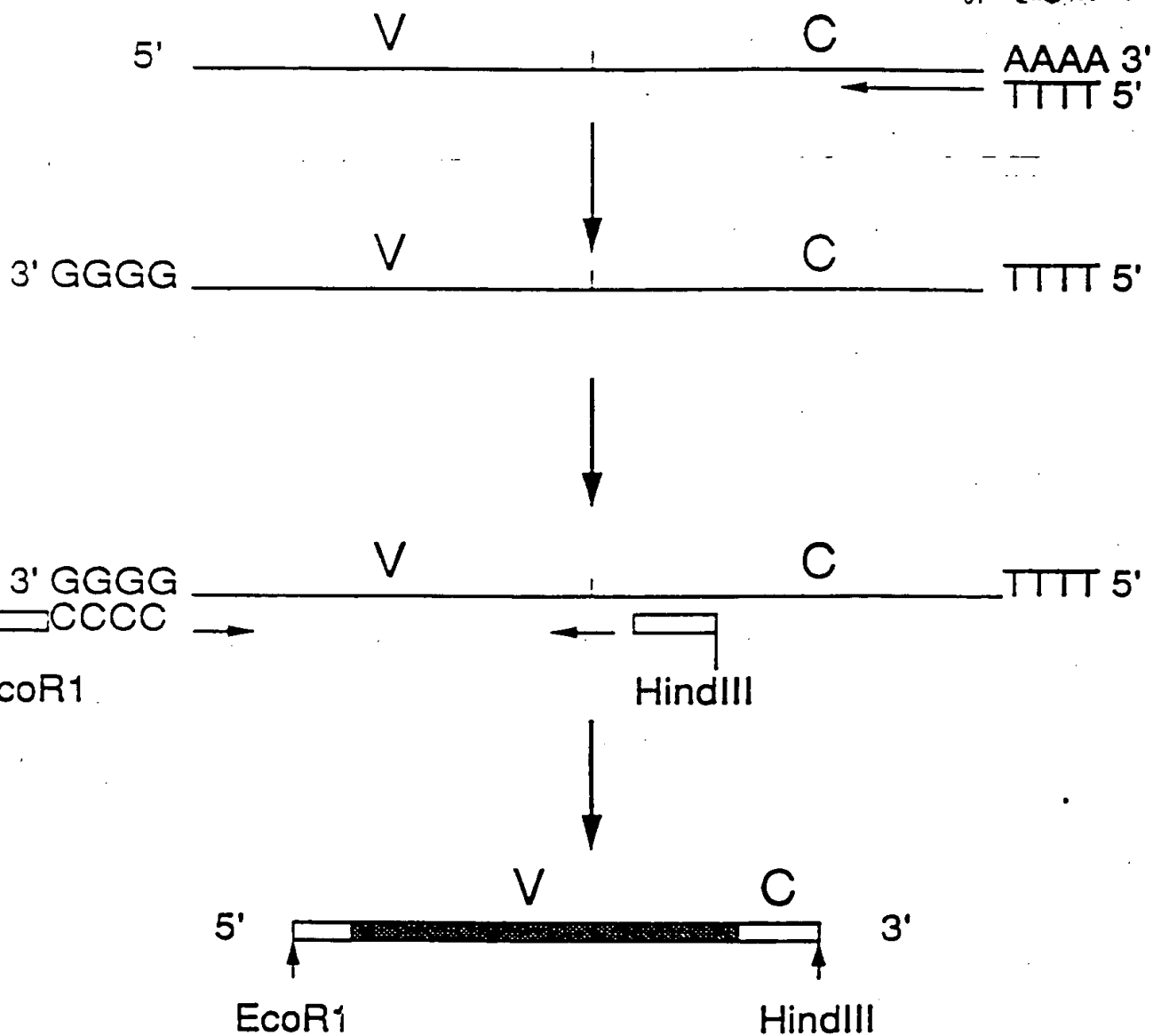


FIGURE 53

07634278

30 60  
 ATGCATCAGACCAGCATGGGCATCAAGATGGAATCACAGACTCTGGTCTTCATATCCATA  
 M H Q T S M G I K M E S Q T L V F I S I

90 120  
 CTGCTCTGGTTATATGGTGCTGATGGGAACATTGTTATGACCCAATCTCCCAAATCCATG  
 L L W L Y G A D G N I V M T Q S P K S M

150 180  
 TACGTGTCAATAGGAGAGAGGGTCACCTTGAGCTGCAAGGCCAGTGAAAATGTGGATACT  
 Y V S I G E R V T L S C K A S E N V D T

210 240  
 TATGTATCCTGGTATCAACAGAAACCAGAGCAGTCTCCTAAACTGCTGATATATGGGGCA  
Y V S W Y Q Q K P E Q S P K L L I Y G A

270 300  
 TCCAACCGGTACACTGGGGTCCACGATCGCTTCACGGGCAGTGGATCTGCAACAGATTTC  
S N R Y T G V H D R F T G S G S A T D F

330 360  
 ACTCTGACCATCAGCAGTGTGCAGGCTGAAGACCTTGCAGATTATCACTGTGGACAGAGT  
 T L T I S S V Q A E D L A D Y H C G Q S

390  
 TACAACTATCCATTACGTTTCGGCTCGGGGACAAAGTTGGAAATAAAG  
Y N Y P F T F G S G T K L E I K

FIGURE 54A

07 634278

30 60  
ATGACATCACTGTTCTCTCTACAGTTACCGAGCACACAGGACCTCGCCATGGGATGGAGC  
M T S L F S L Q L P S T Q D L A M G W S

90 120  
TGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCTCTCCCAGGTCCAAGTGCAG  
C I I L F L V A T A T G V L S Q V Q L Q

150 180  
CAGCCTGGGGCTGACCTTGTGATGCCTGGGGCTCCAGTGAAGCTGTCCTGCTTGGCTTCT  
Q P G A D L V M P G A P V K L S C L A S

210 240  
GGCTACATCTTCACCAGCTCCTGGATAAACTGGGTGAAGCAGAGGCCTGGACGAGGCCTC  
G Y I F T S S W I N W V K Q R P G R G L

270 300  
GAGTGGATTGGAAGGATTGATCCTTCCGATGGTGAAGTTCACCTACAATCAAGATTTCAAG  
E W I G R I D P S D G E V H Y N Q D F K

330 360  
GACAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACATCCAACTCAACAGC  
D K A T L T V D K S S S T A Y I Q L N S

390 420  
CTGACATCTGAGGACTCTGCGGTCTATTACTGTGCTAGAGGATTTCTGCCCTGGTTTGCT  
L T S E D S A V Y Y C A R G F L P W F A

450  
GACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA  
D W G Q G T L V T V S A

FIGURE 54B

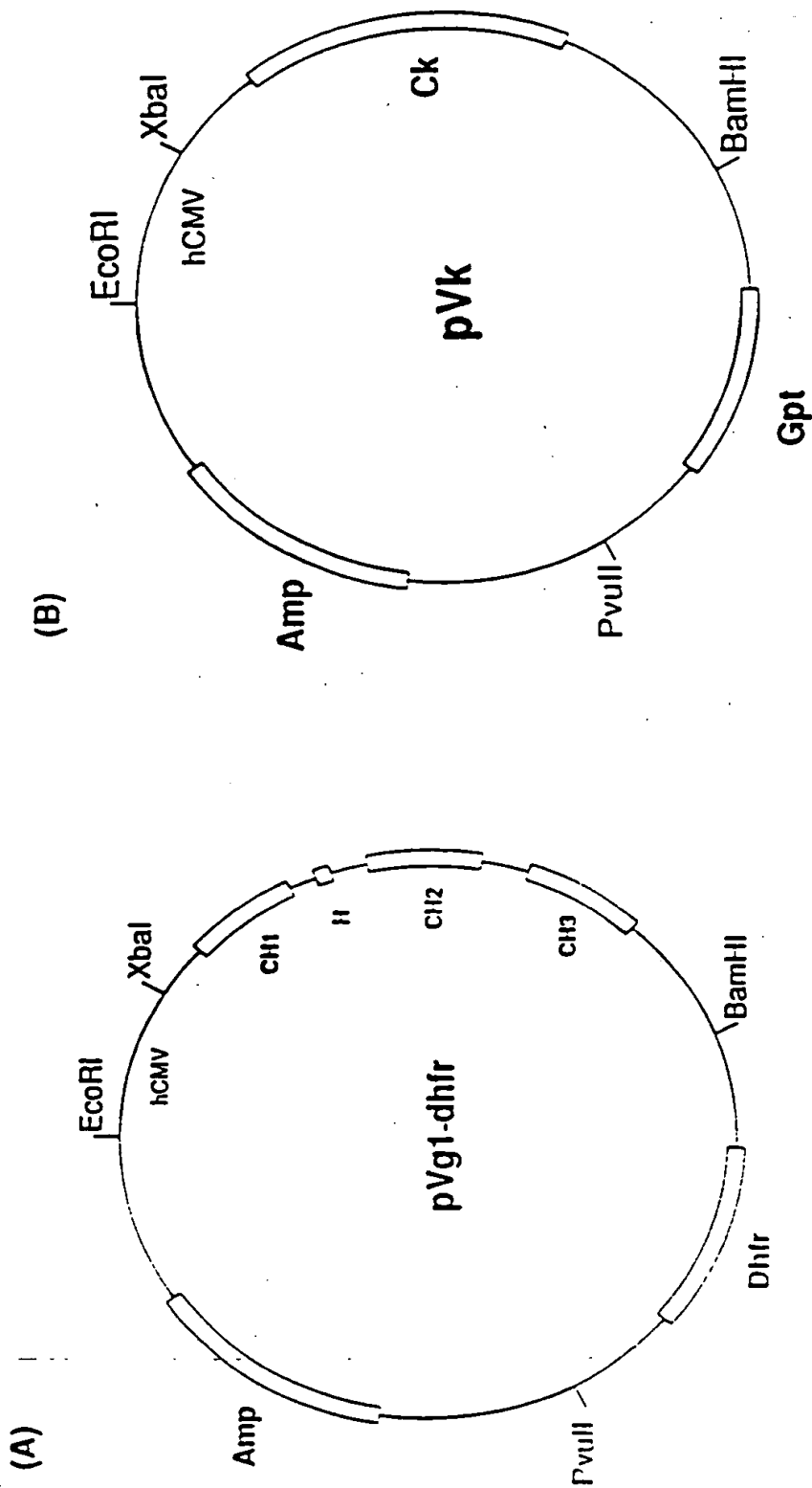


FIGURE 55

07 634278

**A**

1	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	V	T
1	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	V	T
21	I	T	C	R	A	S	Q	S	I	N	T	W	L	A	W	Y	Q	Q	K	P
21	I	T	C	<u>K</u>	<u>A</u>	<u>S</u>	<u>E</u>	<u>N</u>	<u>V</u>	<u>D</u>	<u>T</u>	<u>Y</u>	<u>V</u>	<u>S</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>	<u>P</u>
41	G	K	A	P	K	L	L	M	Y	K	A	S	S	L	E	S	G	V	P	S
41	G	K	A	P	K	L	L	<u>I</u>	<u>Y</u>	<u>G</u>	<u>A</u>	<u>S</u>	<u>N</u>	<u>R</u>	<u>Y</u>	<u>T</u>	<u>G</u>	<u>V</u>	<u>P</u>	<u>S</u>
61	R	F	I	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	P
61	R	F	<u>S</u>	G	S	G	S	G	T	<u>D</u>	F	T	L	T	I	S	S	L	Q	P
81	D	D	F	A	T	Y	Y	C		Q	Q	Y	N	S	D	S	K	M	F	G
81	D	D	F	A	T	Y	Y	C	<u>G</u>	<u>Q</u>	<u>S</u>	<u>Y</u>	<u>N</u>		<u>Y</u>	<u>P</u>	<u>F</u>	<u>T</u>	<u>F</u>	<u>G</u>
100	Q	G	T	K	V	E	V	K												
100	Q	G	T	K	V	E	V	K												

**B**

1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V
1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V
21	S	C	K	A	S	G	G	T	F	S	R	S	A	I	I	W	V	R	Q	A
21	S	C	K	A	S	G	<u>Y</u>	<u>I</u>	<u>F</u>	<u>T</u>	<u>S</u>	<u>S</u>	<u>W</u>	<u>I</u>	<u>N</u>	<u>W</u>	<u>V</u>	<u>R</u>	<u>Q</u>	<u>A</u>
41	P	G	Q	G	L	E	W	M	G	G	I	V	P	M	F	G	P	P	N	Y
41	P	G	Q	G	L	E	W	M	G	<u>R</u>	<u>I</u>	<u>D</u>	<u>P</u>	<u>S</u>	<u>D</u>	<u>G</u>	<u>E</u>	<u>V</u>	<u>H</u>	<u>Y</u>
61	A	Q	K	F	Q	G	R	V	T	I	T	A	D	E	S	T	N	T	A	Y
61	<u>N</u>	<u>Q</u>	<u>D</u>	<u>F</u>	<u>K</u>	<u>D</u>	<u>R</u>	<u>V</u>	<u>T</u>	<u>I</u>	<u>T</u>	<u>A</u>	<u>D</u>	<u>E</u>	<u>S</u>	<u>T</u>	<u>N</u>	<u>T</u>	<u>A</u>	<u>Y</u>
81	M	E	L	S	S	L	R	S	E	D	T	A	F	Y	F	C	A	G	G	Y
81	M	E	L	S	S	L	R	S	E	D	T	A	<u>V</u>	<u>Y</u>	<u>Y</u>	<u>C</u>	<u>A</u>	<u>R</u>	<u>G</u>	<u>F</u>
101	G	I	Y	S	P	E	E	Y	N	G	G	L	V	T	V	S	S			
101	<u>L</u>	<u>P</u>	<u>W</u>	<u>F</u>	<u>A</u>	<u>D</u>	<u>W</u>	<u>G</u>	<u>Q</u>	<u>G</u>	<u>T</u>	<u>L</u>	<u>V</u>	<u>T</u>	<u>V</u>	<u>S</u>	<u>S</u>			

FIGURE 56



07 634278

r10

10 20 30 40 50  
TTTTTCTAG ACCACCATGG AGACCGATAC COTCCTGCTA TGGGTCCCTCC TGCTATGGGT  
70 80 90 100 110  
ACCAGGATCA ACCGGAGATA TTCAGATGAC SCAGTCTCCG TCGACCCCTCT CTGCT

r11

10 20 30 40 50 60  
TTTAAAGCTT GGGAGCTTTG CCTGGCTTCT GCTGATACCA GGATACATAA GTATCCACAT  
70 80 90 100 110 120  
TTCACCTGGC CTTGCAGGTT ATGGTGACCC TATCCCCGAC GCTAGCAGAG AGGGTCGACC

r12

10 20 30 40 50 60  
TTTAAAGCTT CTAATTTATG GGGCATCCAA CCGGTACACT GGGGTACCTT CACGCTTCAG  
70 80 90 100 110  
TGGCAGTGGA TCTGGGACCG ATTTACCCTT CACAATCAGC TCTCTGCAGC CAGATGAT

r13

10 20 30 40 50 60  
TTTTTCTAG AGCAAAAGTC TACTTACGTT TGACCTCCAC CTTGGTCCCC TGACCGAACG  
70 80 90 100 110 120  
TGAATGGATA GTTGTAAGTC TGTCCGAGT AATAAGTGGC GAAATCATCT GGCTGCAGAG

FIGURE 57A

07 634278

rh20

10 20 30 40 50 60  
TTTTTCTAGA CCACCATGGG ATGGAGCTGG ATCTTTCTCT TCCTCCTGTC AGGTACCGCG  
70 80 90 100 110  
GGCGTGCACT CTCAGGTCCA GCTTGTCCAG TCTGGGGCTG AAGTCAAGAA ACCT

rh21

10 20 30 40 50 60  
TTTTGAATTC TCGAGACCCT GTCCAGGGGC CTGCCTTACC CAGTTTATCC AGGAGCTAGT  
70 80 90 100 110 120  
AAAGATGTAG CCAGAAGCTT TGCAGGAGAC CTTACCGGAG CTCCCAGGTT TCTTGACTTC

A

rh22

10 20 30 40 50 60  
TTTTGAATTC TCGAGTGGAT GGGAAGGATT GATCCTTCCG ATGGTGAAGT TCACTACAAT  
70 80 90 100 110 120  
CAAGATTTCA AGGACCGTGT TACAATTACA GCAGACGAAT CCACCAATAC AGCCTACATG  
130  
GAACTGAGCA GCCTGAG

rh23

10 20 30 40 50 60  
TTTTTCTAGA GGTTTTAAGG ACTCACCTGA GGAGACTGTG ACCAGGGTTC CTTGGCCCCA  
70 80 90 100 110 120  
GTCAGCAAAC CAGGGCAGAA ATCCTCTTGC ACAGTAATAG ACTGCAGTGT CCTCTGATCT  
130  
CAGGCTGCTC AGTT

FIGURE 57B

U1 634278

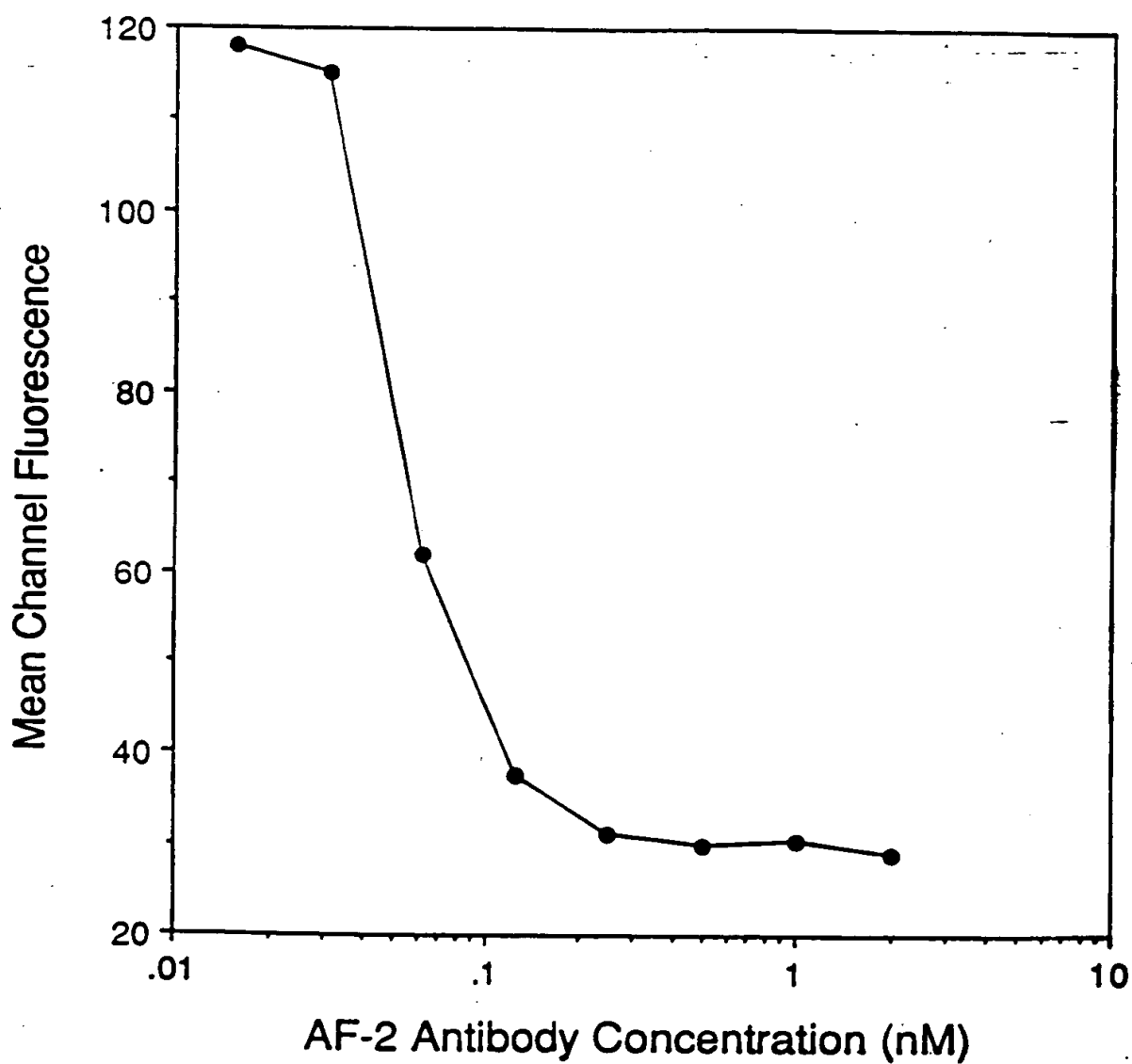


FIGURE 58